

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
819	Y13304	Hylobates hoolock mitochondrial DNA for cytb gene, Horace	0.020	285580	(D10043) ORF [Acetobacter pasteurianus] (U80439) coded for by C. elegans cDNA yk7c8.5; coded for by C. elegans cDNA yk133b3.5; coded for by C. elegans cDNA yk65a4.5; coded for by C. elegans cDNA yk7c8.3; coded for by C. elegans cDNA CEESQ66F; coded for by C. elegans cDNA yk65a4.3;...	2.1
820	Z66539	H.sapiens creatine transporter gene	0.020	1703594	EARLY GROWTH RESPONSE PROTEIN 1 fish >gi 531456 (U12895) egr1 [Danio rerio] rerio]	0.98
821	AF053622	Homo sapiens alpha 1,2-mannosidase IB gene, exon 9	0.020	1352361	HYPOTHETICAL 38.1 KD PROTEIN IN SBCB-HISL INTERGENIC REGION >gi 405956 (U00009) ORF_ID:o349#4; similar to [SwissProt Accession Number P33015] [Escherichia coli] >gi 1736693 gnl PID d1016570 Number P33015] [Escherichia coli] >gi 1788323 (AE000292) putative transport system permease protein [Escherichia coli]	0.72
822	M20555	Human MHC class II HLA-DRw53-beta (DR4,w4) gene, exons 2,3,4,5,6.	0.020	465569	COENZYME PQQ SYNTHESIS PROTEIN F synthesis F - Pseudomonas fluorescens >gi 929802	0.43
823	M20555	Human MHC class II HLA-DRw53-beta (DR4,w4) gene, exons 2,3,4,5,6.	0.020	1709751		0.42

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824	AJ005015	Homo sapiens mRNA for putative SMC-like protein, partial	0.020	267449	HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III >gi 102507 pir S15787 hypothetical protein 1 (cosmid ZK637) - Caenorhabditis elegans GeneFinder; cDNA EST yk217b5.3 comes from this gene; cDNA EST yk217b5.5 comes from this gene; cDNA EST yk340g12.3 comes from this gene; cDNA EST yk340g12.5 comes from this gene; cDNA EST yk428c5.5 co...	1e-12
825	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.020	1109847	(U41538) No definition line found [Caenorhabditis elegans]	1e-22
826	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.019	132836	60S RIBOSOMAL PROTEIN L28 protein L28 [Rattus norvegicus]	5.7
827	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.019	2633401	(Z99109) similar to DNA exonuclease	4.5
828	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.019	2492604	MULTIDRUG RESISTANCE PROTEIN CDR2 [albicans]	4.4
829	U67538	Methanococcus jannaschii section 80 of 150 of the complete genome	0.019	1723566	POTATIVE GLUCOSYLTRANSFERASE C17C9.07 >gi 1314159 gnl PID c241760 (Z73099) SPAC17C9.07, putative glucosyl transferase len: 501, similar to SW:ALG8_YEAST P40351 glucosyltransferase ALG8 pombe]	2.7
830	U56088	Human periodic tryptophan protein 2 (PWP2) gene, exons 3 to 14	0.019	2144804	collagen alpha 1(II) chain - bovine	0.040
831	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.018	1916976	(U91682) vitelline membrane protein homolog [Aedes aegypti]	7.2

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832	AF026258	Onobrychis viciifolia chalcone synthase (CHS) mRNA, complete cds	0.018	763076	(Z48799) ZP3 [Cyprinus carpio] >gi 777724 (L41637) egg membrane protein [Cyprinus carpio]	5.2
833	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.009	3955011	(AJ005438) beta adrenoreceptor B	0.60
834	X71603	C.jejuni VSI DNA >:: emb A39603 A39603 Sequence 2 from Patent WO9417205 >:: gb I76090 I76090 Sequence 2 from patent US 5691138	0.008	<NONE>	<NONE>	<NONE>
835	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.008	138116	HEAD FIBER PROTEIN (LATE PROTEIN GP8.5) >gi 75846 pir WMBP8H gene 8.5 protein - phage PZA >gi 216057 (M11813) head fiber protein	8.1
836	X91751	Bovine herpesvirus type 1 UL7 gene	0.008	1711436	SUPEROXIDE DISMUTASE (FE) 1.15.1.1 (Fe) - Pseudomonas aeruginosa >gi 409767	5.9
837	M95594	Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate synthase (ACS2) gene, complete cds.	0.008	683698	(Z48229) orf1 gene product [Saccharomyces cerevisiae]	1e-06
838	U67465	Methanococcus jannaschii section 7 of 150 of the complete genome	0.008	3874664	(Z68493) predicted using Genefinder	1e-07
839	X72388	B.taurus mRNA for filensin	0.008	100174	1-aminocyclopropane-1-carboxylate synthase	7e-09
840	U22398	Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.	0.008	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	2e-18
841	L42546	Xenopus laevis LIM class homeodomain protein	0.007	<NONE>	<NONE>	<NONE>

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	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
842	AF041428	ribosomal protein s4 X isoform gene, complete cds	0.007	<NONE>	<NONE>	<NONE>
843	AF000227	Secale cereale omega secalin gene, complete cds	0.007	<NONE>	<NONE>	<NONE>
844	D86254	Human MHC (HLA) DRB intron 1 DNA, partial sequence	0.007	<NONE>	<NONE>	<NONE>
845	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
846	Y07738	M.musculus gene for vimentin	0.007	<NONE>	<NONE>	<NONE>
847	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.007	<NONE>	<NONE>	<NONE>
848	AF055119	Homo sapiens alpha-tectorin (TECTA) gene, exon 6	0.007	<NONE>	<NONE>	<NONE>
849	M61195	Zucchini 1-aminocyclopropane-1-carboxylate synthase	0.007	<NONE>	<NONE>	<NONE>
850	Y11050	Homo sapiens DSG3 gene, partial intron and partial exon 6, 140 bp	0.007	<NONE>	<NONE>	<NONE>
851	X61204	M.voltae vhuD, vhuG, vhuA, vhuU & vhuB genes	0.007	<NONE>	<NONE>	<NONE>
852	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.007	<NONE>	<NONE>	<NONE>
853	S43882	telomere: (minichromosome, repeats) [Trypanosoma brucei, Genomic, 1170 nt]	0.007	<NONE>	<NONE>	<NONE>

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	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
854	L32674	Geomydoecus nadleri mitochondrial cytochrome oxidase I gene, partial cds.	0.007	<NONE>	<NONE>	<NONE>
855	U58732	Caenorhabditis elegans cosmid F48D6.	0.007	<NONE>	<NONE>	<NONE>
856	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
857	Z35284	H.sapiens mRNA for MDR3 P-glycoprotein	0.007	1730696	HYPOTHETICAL 121.1 KD PROTEIN IN BIO3-HXT17 INTERGENIC REGION PRECURSOR YNR067c - yeast (Saccharomyces cerevisiae)	9.5
858	X15217	Human sno oncogene mRNA for snoA protein, ski-related	0.007	902455	(U24203) membrane protein [Escherichia coli]	8.8
859	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	1684636	(Y09454) ORF3 [Lactobacillus casei bacteriophage A2]	8.3
860	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	3878803	(Z48795) R05H5.7 [Caenorhabditis elegans]	8.3
861	S76317	119-180-200 kda membrane protein scavenger receptor homolog (clone 18, intron and flanking exons 14 and 15) [sheep, lymph node, lymphocytes, Genomic, 308 nt, segment 2 of 2]	0.007	294747	(L08174) ORF2 [Romanomermis culicivorax]	7.4

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	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
862	D88084	Pedicularis verticillata chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)5'exon	0.007	2555187	(AF026789) vitellogenin [Pimpla nipponica]	6.9
863	X58869	Chicken mRNA for aldehyde dehydrogenase	0.007	115978	CD30L RECEPTOR PRECURSOR (LYMPHOCYTE ACTIVATION ANTIGEN	6.5
864	D87120	Homo sapiens mRNA for GS3786, complete cds	0.007	3879589	(Z50675) Tumor necrosis factor domain, cDNA EST EMBL:D35637 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes fr...	5.1
865	X68793	H.sapiens gene for antithrombin III	0.007	2358285	(AF010403) ALR [Homo sapiens]	3.8
866	AJ001596	Danio rerio mRNA for opioid receptor homologue	0.007	2507509	HYPOTHETICAL 29.8 KD PROTEIN IN HOLB-PTSG INTERGENIC REGION >gi 1787342 (AE000210) orf, hypothetical protein [Escherichia coli] protein in holB 3'region . [Escherichia coli]	1.9
867	AF061195	Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds	0.007	2088768	(AF003145) B0414.8 gene product [Caenorhabditis elegans]	1.9
868	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.007	1710105	UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE UDP-N-acetylglucosamine 2-epimerase [Plasmid pWQ799]	1.7

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	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Zebrafish retinoic acid receptor alpha 2.A	0.007	2239219	(Z97210) hypothetical protein	0.77
869	L03398	Human mRNA for KIAA0150 gene, partial cds	0.007	19917	(Z14014) Pistil extensin like protein, partial CDS only	0.61
870	D63484	Maize glyceraldehyde 3-phosphate dehydrogenase, 3' end.	0.007	543068	mucin, tracheobronchial - dog >gi 402558	0.45
871	M31483	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.007	2494941	ALPHA-2B ADRENERGIC RECEPTOR adrenoceptor [Cavia porcellus] >gi 1587159 prf 2206293B adrenoceptor alpha2B [Cavia porcellus]	0.42
872	AF090115	Helianthus tuberosus lectin I mRNA, complete cds	0.007	1110587	(S79410) nuclear localization signals Peptide, 140 aa [Mus sp.]	0.26
873	AF064029	H.sapiens PAL2A gene	0.007	1706176	CUTINASE TRANSCRIPTION FACTOR 1 ALPHA >gi 1262912 (U51671) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]	0.21
874	X88931	zRAR alpha =retinoic acid receptor alpha [zebrafish, embryos, mRNA, 1773 nt]	0.007	2239219	(Z97210) hypothetical protein	0.11
875	S74155	Petromyzon marinus plasma albumin mRNA, complete cds.	0.007	730888	OCTAPEPTIDE-REPEAT PROTEIN T2	0.011
876	M74193	Saccharomyces cerevisiae Spp41p (SPP41) gene, complete cds.	0.007	3820885	(AL033126) 65G3.k [Drosophila melanogaster]	0.001
877	U03673	Homo sapiens mRNA for Laminin-5 beta3 chain, complete cds	0.007	1235974	(X96713) collagen [Globodera pallida]	3e-06
878	D37766					

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879	AF022388	Cacnorhabditis elegans putative transcription factor MAB-3 (mab-3) gene, complete cds	0.007	3747107	(AF095741) unknown [Rattus norvegicus]	5e-09
880	U89984	Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds	0.007	1890281	(U89984) transformation-sensitive protein homolog	2e-09
881	AB020689	Homo sapiens mRNA for KIAA0882 protein, partial cds	0.007	3880809	(U89984) transformation-sensitive protein homolog (AF022388) similar to R. norvegicus rabGAP domains; cDNA EST EMBL:D34945 comes from this gene; cDNA EST EMBL:D27313 comes from this gene; cDNA EST EMBL:D34829 comes from this gene; cDNA EST EMBL:D27312 comes from this gene; cDNA ... Probable rabGAP domains; cDNA EST EMBL:D34945 comes from this gene; cDNA EST EMBL:D27313 comes from this gene; cDNA EST EMBL:D34829 comes from this gene; cDNA EST EMBL:D27312 comes from this gene; cDNA ...	1e-23
882	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
883	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
884	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>

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885	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
886	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	<NONE>	<NONE>	<NONE>
887	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	<NONE>	<NONE>	<NONE>
888	M80529	Rattus norvegicus ceruloplasmin gene, exon 1 and 5' flank	0.006	<NONE>	<NONE>	<NONE>
889	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.006	99408	hypothetical protein 6 - Chlamydomonas reinhardtii transposon >gi 1360717 gnl PID c33461 reinhardtii]	9.6
890	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.006	4039024	(AF039110) polyprotein [Rubella virus]	9.3
891	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	160533	(M94428) merozoite surface antigen 1 [Plasmodium vivax]	7.5
892	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	4019458	(AF093984) envelope glycoprotein [Human immunodeficiency virus type 1]	7.0
893	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	1916976	(U91682) vitelline membrane protein homolog [Aedes aegypti]	6.8
894	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	102059	promastigote surface antigen-2 (clone 4.6) - Leishmania major (fragment) >gi 9583 (X57135) surface antigen P2 [Leishmania major]	2.4
895	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	3171241	(AF067204) transcription factor BF-1 [Danio rerio]	1.0
896	X99384	M.musculus mRNA for paladin gene	0.003	<NONE>	<NONE>	<NONE>

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897	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.003	<NONE>	<NONE>	<NONE>
898	AE001148	Borrelia burgdorferi (section 34 of 70) of the complete genome	0.003	4160388	(AJ011856) ORF Q0255 [Saccharomyces cerevisiae]	7.6
899	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.003	1709213	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)	1.5
900	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
901	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
902	AF104631	Chlamydomonas reinhardtii light harvesting complex II protein precursor (Lhcb3) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
903	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
904	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>
905	M21339	Human non-histone chromosomal protein HMG-14 gene, complete cds.	0.002	<NONE>	<NONE>	<NONE>
906	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>

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	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human h-lys gene for lysozyme (upstream region)	0.002	<NONE>	<NONE>	<NONE>
907	X57103					
		Sambucus nigra hevein-like protein mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
908	AF074386					
		Human CD4 promoter, partial sequence.	0.002	<NONE>	<NONE>	<NONE>
909	U01066					
		Barley mRNA sequence.	0.002	<NONE>	<NONE>	<NONE>
910	L28094					
		Homo sapiens DNA from chromosome 19-cosmid f19399 (-17 kb EcoRI restriction fragment)	0.002	<NONE>	<NONE>	<NONE>
911	AD000833					
		Homo sapiens TRHR gene promoter and exons 1-2, partial	0.002	<NONE>	<NONE>	<NONE>
912	AJ011701					
		Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
913	AF100694					
		Homo sapiens retinol dehydrogenase gene, complete cds	0.002	<NONE>	<NONE>	<NONE>
914	AF037062					
		Rattus norvegicus homer-1c mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
915	AF093268					
		Methanococcus jannaschii section 150 of 150 of the complete genome	0.002	<NONE>	<NONE>	<NONE>
916	U67608					
		Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
917	AF027173					
		H.sapiens DNA for repeat region (ABM-C82)	0.002	<NONE>	<NONE>	<NONE>
918	Z46736					
		Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>
919	AB012106					

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920	Z85983	X.laevis mRNA for NOVA protein	0.002	<NONE>	<NONE>	<NONE>
921	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
922	S61977	medium-chain acyl-CoA dehydrogenase (exon 10, intron 10) [human, Genomic, 1407 nt]	0.002	<NONE>	<NONE>	<NONE>
923	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	<NONE>	<NONE>	<NONE>
924	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	<NONE>	<NONE>	<NONE>
925	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>
926	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
927	X51646	H.sapiens DNA for dopamine D2 receptor gene	0.002	3329125	(AE001337) Yop C/Gen Secretion Protein D [Chlamydia trachomatis]	9.5
928	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	465762	HYPOTHETICAL 112.1 KD PROTEIN C06G4.1 IN CHROMOSOME III >gil630524 pir S44748 C06G4.1 protein - Caenorhabditis elegans >gil409292 (L25598) homology with vigilin; coded for by C. elegans cDNA GenBank:M88954 (CEL12C9); putative [Caenorhabditis]	8.9
929	U48478	Human skeletal muscle ryanodine receptor gene	0.002	2137221	co-repressor protein - mouse >gil642619	6.9

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		Mus musculus				
930	AF100694	Pontin52 mRNA, complete cds	0.002	806536	(Z22520) membrane protein [Bacillus acidopullulyticus]	6.3
931	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	3881055	(AL023844) Y48A6B.1 [Caenorhabditis elegans]	5.8
932	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.002	3878330	(Z81097) K07A1.4 [Caenorhabditis elegans]	4.8
933	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	137640	REPLICATION PROTEIN E1 papillomavirus	4.0
934	AF019660	Mus musculus nuclear orphan receptor RORgamma	0.002	1330365	(U58757) similar to nucleotide pyrophosphatases	3.9
935	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	1785972	(U46951) ORF5; Method: conceptual translation supplied by author	3.7
936	V00508	Human gene for epsilon-globin.	0.002	1333804	(X56082) protease [Ruminococcus flavefaciens]	3.5
937	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	4153876	(AC005531) similar to mouse homeodomain-interacting protein kinase 2; similar to AF077659 (PID:g3702958)	3.0
938	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	1070461	ornithine carbamoyltransferase (EC 2.1.3.3) - yeast (Saccharomyces cerevisiae) >gi 929866 (X83502) pid:c130025 [Saccharomyces cerevisiae] >gi 1008256	2.8
939	S41458	rod cGMP phosphodiesterase beta-subunit [human, mRNA, 3231 nt]	0.002	3450883	(AF083334) fibroin [Antheraea pernyi]	1.6

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940	X06286	Drosophila melanogaster Gart locus with genes for GARS=phosphoribosylamineglycine ligase, AIRS=phosphoribosylformylglycinamide cyclo-ligase, GART=glycinamide ribotide transformylase > :: gb J02527 DROGART D.melanogaster Gart gene encoding two polypeptides with GAR synthase, AIR synthase, and GAR transformylase enzyme activities and a pupal cuticle gene nested within intron A of the Gart gene.	0.002	2662054	(AB004651) isocitrate lyase	1.5
941	AF015812	Homo sapiens RNA helicase p68 (HUMP68) gene, complete cds	0.002	3641659	(AB008374) alpha 3 type I collagen	1.1
942	X78925	H.sapiens HZF2 mRNA for zinc finger protein	0.002	141624	ZINC FINGER PROTEIN ZFP-37 (MALE GERM CELL SPECIFIC ZINC FINGER PROTEIN)	1.0
943	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	3879997	(Z49071) weak similarity with mu-type opioid receptor (Swiss Prot accession number P33535)	1.0
944	Z69639	Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.	0.002	3523162	(AF076292) TGF-beta/activin signal transducer FAST-1p	0.81

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
945	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	2984161	(AE000761) hypothetical protein [Aquifex aeolicus]	0.80
946	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	101830	hypothetical protein B - chestnut blight fungus	0.72
947	AF017307	Homo sapiens Ets-related transcription factor (ERT) mRNA, complete cds	0.002	200531	(M18071) prion protein [Mus musculus]	0.72
948	U11383	Drosophila melanogaster Ovo-1028aa (ovo) mRNA, complete cds.	0.002	2465207	(AF016045) OVO-like 1 binding protein [Homo sapiens]	0.35
949	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	3834294	(U80846) No definition line found [Caenorhabditis elegans]	0.29
950	AF086315	Homo sapiens full length insert cDNA clone ZD52F10	0.002	545067	(S68356) action potential broadening potassium channel=Shab [Aplysia, bag cell neurons, head ganglia, Peptide, 905 aa] [Aplysia] >gi 743110 prf 2011375A K channel [Aplysia californica]	0.15
951	X53096	S.aureus genes encoding Sau96I DNA methyltransferase and Sau96I restriction endonuclease	0.002	2529575	(AF018164) kinesin-like protein 3C [Homo sapiens]	0.11
952	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	729918	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)	0.092
953	X73973	G.gallus RAR-gamma2 mRNA for retinoic acid receptor	0.002	586122	TRICHOHYALIN >gi 423321 pir A40691 trichohyalin - sheep >gi 295941 (Z18361) trichohyalin	0.073
954	S41458	rod cGMP phosphodiesterase beta-subunit [human, mRNA, 3231 nt]	0.002	1017427	(X90569) elastic titin [Homo sapiens]	0.013

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		D.melanogaster			(U88169) similar to	
955	M35887	defective chorion-1 fc125 (dec-1) gene, complete cds.	0.002	1825606	molybdopterin biosynthesis MOEB proteins [Caenorhabditis elegans]	0.008
956	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.002	1825593	(U88167) D2092.2 gene product [Caenorhabditis elegans]	1e-06
957	AF033929	Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence	9e-04	<NONE>	<NONE>	<NONE>
958	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-04	<NONE>	<NONE>	<NONE>
959	AF029062	Homo sapiens DEAD- box protein (BAT1) gene, partial cds	8e-04	<NONE>	<NONE>	<NONE>
960	U70671	Human ataxin-2 related protein mRNA, partial cds	8e-04	<NONE>	<NONE>	<NONE>
961	AF051709	Dendrocopos leucopterus clone 2 microsatellite HrU2 repeat region	8e-04	<NONE>	<NONE>	<NONE>
962	X14077	Pea phy gene for phytochrome apoprotein	8e-04	<NONE>	<NONE>	<NONE>
963	AC004497	Homo sapiens chromosome 21, P1 clone LBNL#6	8e-04	457146	(L27838) rhopty protein (Plasmodium yoelii)	9.6
964	AF077344	Homo sapiens cartilage-derived C- type lectin	8e-04	3702123	(AJ011707) TraD protein (Escherichia coli)	8.5
965	X85117	H.sapiens epb72 gene exons 2,3,4,5,6,7	8e-04	2570059	(AJ004687) N-4 cytosine- specific methyltransferase (Neisseria gonorrhoeae)	6.8
966	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	1345859	COPPER TRANSPORT PROTEIN CTR1 transport protein - yeast (Saccharomyces cerevisiae) gene product [Saccharomyces cerevisiae]	6.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
967	AF031403	MLL/AF4 translocation breakpoint t(4;11)(q21;23)	8e-04	2498926	SMALL PROTEIN B HOMOLOG A43259, from E. hirae [Mycoplasma pneumoniae]	6.6
968	L29252	Human (clone D13-2) L-iditol-2 dehydrogenase gene, exon 4, exon 5, exon 6 and exon 7.	8e-04	1488070	(U63997) putative transposase [Enterococcus faecium]	5.2
969	X16995	Mouse N10 gene for a nuclear hormonal binding receptor	8e-04	1493833	(U47323) stromal cell protein [Mus musculus]	3.2
970	M99412	Human interleukin-8 receptor (IL8RB) gene, complete cds	8e-04	1346101	4-AMINOBUTYRATE AMINOTRANSFERASE TRANSAMINASE) (GABA AMINOTRANSFERASE) homolog - smut fungus (Ustilago maydis) >gi 881562 Emericella nidulans gamma-amino-n-butyrate transaminase Swiss-Prot Accession Number P14010 [Ustilago maydis]	0.83
971	U37452	Human Down Syndrome region of chromosome 21 genomic sequence, clone A31D6-1C5.	8e-04	4164069	(AF111093) latrophilin 3 splice variant bbah [Bos taurus]	0.26
972	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	1352877	HYPOTHETICAL 13.0 KD PROTEIN IN RAD26-GEF1 INTERGENIC REGION >gi 1077881 pir S57057 probable membrane protein YJR038c - yeast (Saccharomyces cerevisiae) >gi 1015688 (Z49538) ORF YJR038c putative [Saccharomyces cerevisiae]	0.23
973	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-04	1788557	(AE000312) orf, hypothetical protein [Escherichia coli]	0.19

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
974	X83872	H.vulgaris mRNA for cAMP response element binding protein	8e-04	1175386	HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I >gi 2130289 pir S58305 hypothetical protein SPAC18B11.06 - fission yeast hypothetical protein [Schizosaccharomyces pombe]	0.005
975	M32514	Rat simple sequence DNA, clone 5.	8e-04	2394492	(AF024502) No definition line found [Caenorhabditis elegans]	0.002
976	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-04	2981631	(AB012223) ORF2 [Canis familiaris]	0.001
977	X89211	H.sapiens DNA for endogenous retroviral like element	8e-04	2065210	(Y12713) Pro-Pol-dUTPase polypeptide	3e-04
978	U14391	Human myosin-1C mRNA, complete cds.	8e-04	3142302	(AC002411) Strong similarity to myosin heavy chain gb Z34293 from A. thaliana. [Arabidopsis thaliana]	4e-16
979	L13612	Drosophila melanogaster dead-box protein D.melanogaster DEAD-box gene, complete CDS	8e-04	3776027	(AJ010475) RNA helicase [Arabidopsis thaliana]	9e-24
980	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
981	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
982	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
983	Z73987	Human DNA sequence from cosmid N120B6 on chromosome 22 Contains ESTs, complete sequence [Homo sapiens]	7e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Brassica rapa mRNA for SRK45, complete cds	7e-04	<NONE>	<NONE>	<NONE>
984	AB012106					
985	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
986	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
987	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
988	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	<NONE>	<NONE>	<NONE>
989	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
990	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
991	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
992	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
993	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
994	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	3327230	(AB014608) KIAA0708 protein [Homo sapiens]	9.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
995	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	3327230	(AB014608) KIAA0708 protein [Homo sapiens]	9.3
996	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	3876455	(Z93380) predicted using Genefinder; similar to 7tm receptor protein [Caenorhabditis elegans]	7.1
997	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	2128771	hypothetical protein MJ1293 - Methanococcus jannaschii >gi 1591931 (U67570) M. jannaschii predicted coding region MJ1293 [Methanococcus jannaschii]	6.2
998	U09412	Human zinc finger protein ZNF134 mRNA, complete cds	7e-04	1083336	glutathione transferase (EC 2.5.1.18) piA - mouse	5.4
999	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	473515	(M17619) NADH dehydrogenase subunit ND4 [Asterina pectinifera]	3.7
1000	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	1724097	(U79772) female sex protein [Mercurialis annua]	3.3
1001	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	1197103	(D49747) core, env, and part of E2/NS1	3.2
1002	X16995	Mouse N10 gene for a nuclear hormonal binding receptor	7e-04	345372	unc-5 protein, long form - Caenorhabditis elegans >gi 258529 bbs 118648 (S47168) UNC-5=immunoglobulin and thrombospondin type 1 transmembrane protein {alternatively spliced} aa [Caenorhabditis elegans] >gi 2662596 (AF036698) C. elegans UNC-5 (NID:g25852)	2.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1003	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	4204220	(AB022866) mobilization protein	2.5
1004	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	3201550	(Y17116) fibrinogen-binding protein	2.4
1005	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	1174264	(U45966) polyprotein [Hepatitis G virus]	0.73
1006	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	135308	TRANSCRIPTION FACTOR JUN-D	0.065
1007	X98745	H.sapiens EWS gene, intron 6, polymorphism	7e-04	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.001
1008	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	1633564	(U47924) C8 [Homo sapiens]	9e-09
1009	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	6e-04	284171	Ig epsilon chain C region form 3 - human	1.3
1010	AB012106	Brassica rapa mRNA for SRK45, complete cds	6e-04	3845262	(AE001414) BRAHMA ortholog (DNA helicase superfamily II)	0.25
1011	AL034404	Human DNA sequence from clone 417C12 on chromosome Xp22.11 22.2, complete sequence [Homo sapiens]	3e-04	<NONE>	<NONE>	<NONE>
1012	M99701	Homo sapiens (pp21) mRNA, complete cds.	3e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1013	U00227	Ovis aries Merino breed DR beta-chain antigen binding domain, MHC class II DRB (Ovar-DRB24) gene, partial cds.	3e-04	<NONE>	<NONE>	<NONE>
1014	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1015	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-04	999418	(L19655) ORF [Tomato ringspot virus]	8.3
1016	AB012106	Brassica rapa mRNA for SRK45, complete cds	3e-04	2367460	(AF011415) putative pheromone receptor [Mus musculus]	7.0
1017	AJ010737	Mus musculus DNA for microsatellite 3kb upstream lbp gene	3e-04	4106549	(AF104411) neuronal-specific septin 3 [Mus musculus]	5.5
1018	AF053137	Homo sapiens histone deacetylase 3 gene, exons 4, 5, 6, 7, 8, 9, and 10	3e-04	416702	NADH-DEPENDENT FLAVIN OXIDOREDUCTASE acid-inducible - Eubacterium sp >gi 1381570 (U57489) NADH:flavin oxidoreductase [Eubacterium sp. VPI 12708]	5.3
1019	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	3e-04	1785789	(Y08502) orf111d [Arabidopsis thaliana]	5.1
1020	AC004173	Homo sapiens clone UWGC:y23x011 from 6p21, complete sequence [Homo sapiens]	3e-04	558521	(D28917) polyprotein [Hepatitis C virus]	1.1
1021	X57025	Human IGF-I mRNA for insulin-like growth factor I	3e-04	4206707	(AF118122) putative outer membrane protein OmpU	0.65
1022	X77090	H. sapiens IL-1Ra gene.	3e-04	1065941	(U40799) F42C5.7 gene product [Caenorhabditis elegans]	0.12

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1023	M34651	Pseudorabies virus with upstream and downstream sequences.	3e-04	2746853	(AF040650) contains similarity to sodium-potassium-chloride cotransport proteins	7e-05
1024	Z36011	S.cerevisiae chromosome II reading frame ORF YBR142w	3e-04	2500537	PROBABLE ATP-DEPENDENT RNA HELICASE HAS1 >gi 626265 pir S47451 hypothetical protein YMR290c RNA helicase [Saccharomyces cerevisiae]	4e-08
1025	AF020286	Dictyostelium discoideum 2034 gene, partial cds	3e-04	1465834	(U64857) No definition line found [Caenorhabditis elegans]	6e-14
1026	L26049	Chlamydomonas reinhardtii dynein heavy chain alpha (ODA11) gene, exons 2-15, and partial cds.	3e-04	3876775	(Z81077) predicted using Genefinder; Similarity to Yeast protein 8248 (TR:G587531)	9e-15
1027	AF020286	Dictyostelium discoideum 2034 gene, partial cds	3e-04	1465834	(U64857) No definition line found [Caenorhabditis elegans]	1e-17
1028	X79811	S.cerevisiae ACT3 gene	3e-04	3876090	(Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-31
1029	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1030	M22970	Human pancreatic phospholipase A-2 (PLA-2) gene, exons 1 to 3.	2e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1031	Z68686	Human DNA sequence from cosmid N2E9 on chromosome 22. Contains EST, complete sequence (Homo sapiens)	2e-04	<NONE>	<NONE>	<NONE>
1032	X95154	H.sapiens brca2 gene exon 4 > :: emb A62779 A62779 Sequence 20 from Patent WO9719110	2e-04	<NONE>	<NONE>	<NONE>
1033	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	<NONE>	<NONE>	<NONE>
1034	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1035	AE001415	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence	2e-04	<NONE>	<NONE>	<NONE>
1036	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1037	AC000958	Homo sapiens (subclone 6_d9 from P1 H21) DNA sequence	2e-04	<NONE>	<NONE>	<NONE>
1038	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	2e-04	2501523	CD59 GLYCOPROTEIN PRECURSOR	7.1
1039	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	2765360	(Y13925) cathepsin L2 [Penaeus vannamei]	6.8

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					RNA POLYMERASE	
1040	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	2e-04	133636	>gi 67126 pir RRXPLC RNA-directed RNA polymerase (EC 2.7.7.48) - lymphocytic choriomeningitis virus (strain Armstrong 53b) >gi 331369 (AF074613) type II secretion protein [Escherichia coli O157:H7]	5.2
1041	AB012106	Brassica rapa mRNA for SRK45, complete cds	2e-04	3822155		4.0
1042	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	1718125	REGULATORY PROTEIN E2 >gi 1020222 type 36]	0.38
1043	X17058	Sus scrofa mRNA for glucose transport protein	2e-04	3341906	(AB009593) xylose transporter	2e-15
1044	AF008216	Homo sapiens candidate tumor suppressor pp32r1	1e-04	<NONE>	<NONE>	<NONE>
1045	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	1e-04	624126	(U42580) a65L [Paramecium bursaria Chlorella virus 1]	7.9
1046	L14930	Glycine max (Rab7p) mRNA, complete cds.	9e-05	<NONE>	<NONE>	<NONE>
1047	AJ009970	Mus musculus thromboxane A2 receptor gene, exon 3, partial	9e-05	<NONE>	<NONE>	<NONE>
1048	Y11896	M.musculus mRNA for Brx gene, partial	9e-05	<NONE>	<NONE>	<NONE>
1049	L10832	Polistes annularis (clone pan48AAT) tandem repeat region.	9e-05	<NONE>	<NONE>	<NONE>
1050	AF055011	Homo sapiens clone 24587 mRNA sequence	9e-05	3880586	(Z19758) cDNA EST EMBL:D28009 comes from this gene; cDNA EST EMBL:D28008 comes from this gene; cDNA EST EMBL:D32478 comes from this gene; cDNA EST EMBL:D34508 comes from this gene; cDNA EST EMBL:D37581 comes from this gene; ...	7.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1051	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-05	3024292	RHODOPSIN >gi 2290717 (AF000947) rhodopsin [Sepia officinalis]	6.7
1052	Z58294	H.sapiens CpG DNA, clone 34d6, forward read cpg34d6.ft1a.	9e-05	3885496	(AF064825) heparin/heparan sulfate N-acetylglucosaminyl N-deacetylase/N-sulfotransferase [Bos taurus]	0.65
1053	D87451	Human mRNA for KIAA0262 gene, complete cds	9e-05	3874739	(Z66495) similar to claustrin like	0.004
1054	L37092	Mus musculus cyclin-dependent kinase homologue	9e-05	3080513	(AL022598) hypothetical protein	4e-09
1055	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1056	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1057	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1058	D10102	Homo sapiens DNA from cosmid clone:844, GT repeat sequence	8e-05	<NONE>	<NONE>	<NONE>
1059	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	8e-05	1176475	HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION >gi 1078237 pir S56849 probable membrane protein YJL073w - yeast (Saccharomyces cerevisiae) >gi 895898 (X88851) hypothetical protein YJL073w [Saccharomyces cerevisiae]	6.0
1060	X71934	H.sapiens XB gene for tenascin-X, repeat XIII	8e-05	285207	microtubule-associated protein, 110K tau - rat >gi 207158 (M84156) big tau [Rattus norvegicus]	3.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1061	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	4049682	(AF063866) ORF MSV092 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	2.1
1062	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	8e-05	3861019	(AJ235271) unknown [Rickettsia prowazekii]	5e-14
1063	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-05	<NONE>	<NONE>	<NONE>
1064	L04193	Human lens membrane protein (mp19) gene, exon 11.	7e-05	<NONE>	<NONE>	<NONE>
1065	X61609	B.napus gene for LHC II Type III chlorophyll a/b binding protein	7e-05	2132314	hypothetical protein YPR174c - yeast similarity to a nuclear lamin from C. elegans (PIR accession number S42257) [Saccharomyces cerevisiae]	8.9
1066	AF064029	Helianthus tuberosus lectin I mRNA, complete cds	7e-05	2979422	(AB006757) PCDH7 (BH-Pcdh)c [Homo sapiens]	5.7
1067	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-05	2493696	HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi 1480440 (U34204) ORF185; hypothetical 21.4 kD protein [Brassica oleracea]	5.2
1068	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-05	2501029	PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (LEUCINE--TRNA LIGASE) (LEURS) KIAA0028 [Homo sapiens]	1.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1069	Z68758	Human DNA sequence from cosmid cN85E10 on chromosome 22q11.2-qter	3e-05	<NONE>	<NONE>	<NONE>
1070	X60653	human Histone H3.3 pseudogene (CIR-456)	3e-05	<NONE>	<NONE>	<NONE>
1071	Z58294	H.sapiens CpG DNA, clone 34d6, forward read cpg34d6.ft1a.	3e-05	1706241	GUANYLYL CYCLASE GC-E PRECURSOR cyclase receptor [Mus musculus]	9.6
1072	AF043251	Homo sapiens mitochondrial outer membrane protein (Tom40) gene, nuclear gene encoding mitochondrial protein, exons 1 through 6	3e-05	113980	AMINE OXIDASE [FLAVIN-CONTAINING] B oxidase (flavin-containing) (EC 1.4.3.4) B - human B [human, platelet, Peptide Partial, 520 aa] [Homo sapiens]	8.9
1073	M31104	Chicken progesterone receptor gene, encoding forms A and B, exons 1 and 2.	3e-05	1170841	IG GAMMA LAMBDA CHAIN V-II REGION	4.8
1074	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	543684	ribosomal protein S3 - Chlamydomonas humicola chloroplast (fragment)	4.2
1075	L22206	Human vasopressin receptor V2 gene, complete cds.	3e-05	791207	(U20615) Gnot1 homeodomain protein [Gallus gallus]	1.8
1076	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	3e-05	3237340	(AF033361) polyprotein [Hepatitis C virus]	0.94
1077	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	2879805	(AL021813) hypothetical protein	0.001
1078	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	3877951	(Z81555) predicted using Genefinder	3e-07

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1079	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-05	<NONE>	<NONE>	<NONE>
1080	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	3880197	(Z81132) predicted using Genefinder	2.4
1081	AF087989	Homo sapiens full length insert cDNA clone YX29D10	2e-05	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	1.8
1082	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	474896	(L31967) mating type protein [Coprinus cinereus]	1.4
1083	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	2266988	(Y13274) M33 polycomb-like protein [Mus musculus]	0.62
1084	U67415	Equus caballus UCD-E-CA-467 dinucleotide repeat region, complete sequence	1e-05	<NONE>	<NONE>	<NONE>
1085	X67277	H.sapiens BGP gene for biliary glycoprotein, promoter region and exon 1	1e-05	<NONE>	<NONE>	<NONE>
1086	X85117	H.sapiens epb72 gene exons 2,3,4,5,6,7	1e-05	<NONE>	<NONE>	<NONE>
1087	U88328	Mus musculus suppressor of cytokine signalling-3	1e-05	443877	(Z29457) core region; pid:g443877 [Hepatitis C virus] virus]	3.9
1088	Y12853	Homo sapiens P2X7 gene, exon 4-8	1e-05	3878726	(Z66498) similar to cuticle collagen; cDNA EST EMBL:D75584 comes from this gene	0.36
1089	AE001140	Borrelia burgdorferi (section 26 of 70) of the complete genome	1e-05	3860719	(AJ235270) GLUTAMYL-tRNA AMIDOTRANSFERASE SUBUNIT A (gatA) [Rickettsia prowazekii]	4e-15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1090	AJ224112	Homo sapiens gamma adaptin gene, exon 2 and flanking intronic sequences	9e-06	<NONE>	<NONE>	<NONE>
1091	AB000565	Homo sapiens DNA for repeat sequence Alu	9e-06	72879	translation initiation factor IF-2 - Escherichia coli	5.1
1092	Z78985	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20B4	9e-06	159975	(M65164) 51C surface protein [Paramecium tetraurelia]	4.8
1093	Z21677	Thermotoga maritima DNA for spc operon	9e-06	585879	50S RIBOSOMAL PROTEIN L2 maritima >gi 437926 (Z21677) ribosomal protein L2	7e-14
1094	AF031494	Drosophila hydei Dhc7 (Threads) mRNA, complete cds	9e-06	729377	DYNEIN BETA CHAIN, CILIARY sea urchin (Anthocidaris crassispina) chain [Anthocidaris crassispina]	4e-18
1095	AF051315	Homo sapiens placental protein 17a1 (PP17) mRNA, complete cds	4e-06	<NONE>	<NONE>	<NONE>
1096	AC001460	Homo sapiens (subclone 2_f4 from BAC H107) DNA sequence	4e-06	2648304	(AE000952) ISA1214-6, putative transposase	6.2
1097	X85030	H.sapiens mRNA for skeletal muscle-specific calpain	4e-06	4239857	(AB016726) calpain [Schistosoma japonicum]	0.006
1098	M75162	Human polymorphic arylamine N-acetyltransferase	3e-06	<NONE>	<NONE>	<NONE>
1099	AB009999	Rattus norvegicus mRNA for CDP-diacylglycerol synthase, complete cds	3e-06	3879045	(Z70309) R102.6 [Caenorhabditis elegans]	7.3
1100	Z78985	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20B4	3e-06	266529	MERCURIC REDUCTASE (HG(II) REDUCTASE) >gi 418744 pir S30168 mercury(II) reductase	6.5
1101	AB012190	Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds	3e-06	3877938	(Z79697) F58H10.1 [Caenorhabditis elegans]	6.3

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1102	AF041056	WSCR4 gene, exons 3 and 4	3e-06	1568583	(Z80775) hypothetical protein Rv0044c	1.9
1103	X00777	Mouse E(d) beta gene 5' flanking region and exon 1	3e-06	1680722	(U72497) fatty acid amide hydrolase [Rattus norvegicus]	0.008
1104	D21205	Human mRNA for estrogen responsive finger protein, complete cds	3e-06	563127	(U09825) acid finger protein [Homo sapiens]	1e-05
1105	Z47046	Human cosmid QLL2C9 from Xq28	1e-06	<NONE>	<NONE>	<NONE>
1106	L26261	Human MHC class III HLA-RP1 gene.	1e-06	<NONE>	<NONE>	<NONE>
1107	M13402	Rat 5S RNA gene, clone 5S-2.	1e-06	<NONE>	<NONE>	<NONE>
1108	X68793	H.sapiens gene for antithrombin III	1e-06	<NONE>	<NONE>	<NONE>
1109	AF003540	Homo sapiens Krueppel family zinc finger protein	1e-06	2507553	ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) Kruppel-related. [Homo sapiens]	0.098
1110	L42096	Homo sapiens (subclone 10_d2 from P1 H21) DNA sequence.	1e-06	1330401	(U58762) T27F7.1 gene product [Caenorhabditis elegans]	0.015
1111	Z69925	Human DNA sequence from cosmid cN116A5, between markers D22S280 and D22S86 on chromosome 22q12 contains EST	9e-07	<NONE>	<NONE>	<NONE>
1112	D90217	S. cerevisiae gene for Yml33, mitochondrial ribosomal proteins of large subunit	9e-07	3879097	(Z81109) predicted using Genefinder; similar to sodium/phosphate transporter; cDNA EST yk326f6.3 comes from this gene; cDNA EST yk326f6.5 comes from this gene [Caenorhabditis elegans]	7.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1113	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-07	1330345	(U58755) coded for by C. elegans cDNA yk3461.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	2e-29
1114	AF086562	Homo sapiens full length insert cDNA clone ZE16C03	4e-07	1072210	(U40945) coded for by C. elegans cDNA yk74b9.3; coded for by C. elegans cDNA yk74b9.5; similar to repeat of calcium channel alpha subunits; similar to tetracycline resistance protein; similar to hypothetical protein in HSP30-PMP1 region (SP...	3.9
1115	L39062	Homo sapiens interleukin 9 receptor IL9R pseudogene, exons 1-9	4e-07	3879983	(Z46795) similar to transforming protein etc2; cDNA EST EMBL:D34137 comes from this gene; cDNA EST EMBL:D37172 comes from this gene; cDNA EST EMBL:D76266 comes from this gene; cDNA EST EMBL:D70493 comes from this gene; cDNA ...	3.3
1116	Z69364	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST and cDNA. > :: emb[Z69365][HSL96F8A Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST and cDNA.	4e-07	3493176	(AF022889) latent TGF beta binding protein [Mus musculus]	3.0

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1117	D79986	Human mRNA for KIAA0164 gene, complete cds	4e-07	4038031	(AC005936) hypothetical protein [Arabidopsis thaliana]	0.30
1118	D43950	Human mRNA for KIAA0098 gene, partial cds	3e-07	<NONE>	<NONE>	<NONE>
1119	AF037168	Arabidopsis thaliana DnaJ homologue (AtJ6) mRNA, complete cds	3e-07	3881075	(AL032657) predicted using Genefinder; similar to DnaJ domain ; Thioredoxin; cDNA EST yk433f3.5 comes from this gene; cDNA EST EMBL:D32359 comes from this gene; cDNA EST EMBL:D34721 comes from this gene; cDNA EST yk433f3.3 c...	3e-09
1120	X69838	H.sapiens mRNA for G9a	3e-07	3873414	(U00043) similar to D. melanogaster trithorax protein	3e-29
1121	AB011124	Homo sapiens mRNA for KIAA0552 protein, complete cds	2e-07	2618749	(U90880) hypothetical protein 2; predicted using XGrail	2.0
1122	K03012	Human cellular fms proto-oncogene, partial cds.	1e-07	<NONE>	<NONE>	<NONE>
1123	AB016195	Homo sapiens DNA, microsatellite and Alu repeat region	1e-07	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.095
1124	Y16795	Homo sapiens psihHaA pseudogene	4e-08	<NONE>	<NONE>	<NONE>
1125	AB012624	Homo sapiens FLII gene for ERGB transcription factor, intron 4 and partial cds	4e-08	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	3.6
1126	AJ131341	Homo sapiens ogg1 gene, exons 1-7	4e-08	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	3e-05
1127	L81902	Homo sapiens (subclone 1_c10 from P1 H69) DNA sequence	3e-08	4225950	(AJ132701) centaurin gamma1B	1.8
1128	Y17968	Gallus gallus mRNA for high mobility group 1 protein	3e-08	3041855	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) (Homo sapiens)	3e-31
1129	Y13901	Homo sapiens FGFR-4 gene	1e-08	<NONE>	<NONE>	<NONE>

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1130	L22024	Mesocricetus auratus serum amyloid P component gene, complete cds.	1e-08	<NONE>	<NONE>	<NONE>
1131	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	1e-08	<NONE>	<NONE>	<NONE>
1132	X14034	Human mRNA for phospholipase C > :: gb M37238 HUMPL C Human phospholipase C mRNA, complete cds.	1e-08	<NONE>	<NONE>	<NONE>
1133	Z59381	H.sapiens CpG DNA, clone 152b10, forward read cpg152b10.ft1a.	1e-08	<NONE>	<NONE>	<NONE>
1134	L81839	Homo sapiens (subclone 2_h3 from P1 H43) DNA sequence	1e-08	<NONE>	<NONE>	<NONE>
1135	X14448	Human GLA gene for alpha-D-galactosidase A (EC 3.2.1.22)	1e-08	3334427	HYPOTHETICAL PROTEIN MJ1207 Methanococcus jannaschii >gi 1591837 (U67562) protease synthase and sporulation negative regulator Pail, putative [Methanococcus jannaschii]	9.1
1136	AL023774	Human DNA sequence from clone 799F15 on chromosome Xq25, complete sequence [Homo sapiens]	1e-08	1354935	(U58330) probable copper-transporting atpase	1.2
1137	X64639	H.sapiens DNA repetitive subtelomeric-like sequence (522 bp)	1e-08	77356	hypothetical 70K protein - eggplant mosaic virus	0.098
1138	U97058	Human HuD gene, 5'UTR	5e-09	3387886	(AF070530) unknown [Homo sapiens]	9.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1139	Z82181	sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	5e-09	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	8.4
1140	AJ006587	Mus musculus mRNA for translation initiation factor eIF2 gamma X	5e-09	1872200	(U22376) alternatively spliced product using exon 13A	0.64
1141	Y11108	H.sapiens WNT8B gene	4e-09	2854198	(AF045646) contains similarity to collagens	4.0
1142	AE001223	Treponema pallidum section 39 of 87 of the complete genome	4e-09	3334189	CELL DIVISION PROTEIN FTSY HOMOLOG	1.5
1143	Z47046	Human cosmid QLL2C9 from Xq28	4e-09	104045	fibroblast growth factor receptor A1 precursor - African clawed frog >gi 214894 (M55163) fibroblast growth factor receptor [Xenopus laevis]	1.3
1144	AG000746	Homo sapiens genomic DNA, 21q region, clone: T171Bm40	4e-09	113666	!!!! ALU CLASS A WARNING ENTRY !!!! (Z56748) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes f... >gi 3878699 gnl PID e1351700 possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes f...	0.33
1145	M74002	Human arginine-rich nuclear protein mRNA, complete cds.	4e-09	3875371		3e-06
1146	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-09	2494337	ENDO-1,4-BETA-XYLANASE PRECURSOR sp.]	4.9

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					UDP-	
1147	U20554	Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.	2e-09	2499087	GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) glucosyltransferase - fruit fly (Drosophila sp.) glucosyltransferase precursor [Drosophila melanogaster]	4e-24
1148	Z56162	H.sapiens CpG DNA, clone 91c9, forward read cpg91c9.ft1a.	1e-09	<NONE>	<NONE>	<NONE>
1149	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-09	1002424	(U25739) YSPL-1 form 1 [Mus musculus]	8.9
1150	M85276	Homo sapiens NKG5 gene, complete cds.	1e-09	2315436	(AF016447) No definition line found [Caenorhabditis elegans]	8.3
1151	M94065	Human dihydroorotate dehydrogenase mRNA, 3' end.	1e-09	3892656	(AB014464) MGC-24v [Mus musculus]	6.2
1152	AJ131895	Homo sapiens genomic CAG repeat element, clone 60o2(250)	5e-10	<NONE>	<NONE>	<NONE>
1153	Z82181	Human DNA sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	5e-10	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	7.9
1154	AJ224442	Homo sapiens mRNA for putative methyltransferase	5e-10	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.15
1155	AJ010230	Homo sapiens RET finger protein-like 1 antisense transcript, partial	5e-10	728834	!!!! ALU SUBFAMILY SB2 WARNING ENTRY	0.006
1156	AF111116	Homo sapiens silencer of death domains (SODD) mRNA, complete cds	5e-10	4160014	(AF111116) silencer of death domains [Homo sapiens]	2e-08
1157	Z97017	Homo sapiens mRNA for hypothetical protein	4e-10	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens type II integral membrane protein				
1158	AF001298		4e-10	<NONE>	<NONE>	<NONE>
1159	Y11395	H.sapiens mRNA for p40	2e-10	1000340	(U34384) CheW [Borrelia burgdorferi]	2.4
1160	U41096	Human non-coding sequence upstream from DOC-2 gene on chromosome 5	2e-10	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.28
1161	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	6e-11	<NONE>	<NONE>	<NONE>
1162	Z36111	S.cerevisiae chromosome II reading frame ORF YBR242w	6e-11	2213560	(Z97052) hypothetical protein (Z80220) Similarity to yeast protein TREMBL ID E246895); cDNA EST EMBL:T00018 comes from this gene; cDNA EST EMBL:C13908 comes from this gene; cDNA EST EMBL:C11656 comes from this gene; cDNA EST yk234a5.3 comes from this ge...	3e-27
1163	D89174	Schizosaccharomyces pombe mRNA, partial cds, clone: SY 1004	6e-11	3879758		4e-30
1164	Z95437	Human DNA sequence from cosmid A1 on chromosome 6 contains ESTs. HERV like retroviral sequence	5e-11	<NONE>	<NONE>	<NONE>
1165	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	5e-11	3886065	(AF106581) contains similarity to C4-type zinc fingers	4.9
1166	X56997	Human Uba52 gene coding for ubiquitin-52 amino acid fusion protein	2e-11	<NONE>	<NONE>	<NONE>
1167	AF086253	Homo sapiens full length insert cDNA clone ZD40G12	2e-11	2134780	apoptosis inhibitor IAP homolog - human	3.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1168	AB018314	Homo sapiens mRNA for KIAA0771 protein, partial cds	2e-11	3024343	P53-BINDING PROTEIN 53BP2 Bbp/53BP2 [Homo sapiens]	2e-11
1169	Z74972	S.cerevisiae chromosome XV reading frame ORF YOR064c	2e-11	3041855	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	2e-40
1170	Z82181	Human DNA sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	7e-12	<NONE>	<NONE>	<NONE>
1171	X77738	H.sapiens red cell anion exchanger (EPB3, AE1, Band 3) gene, 3' region	7e-12	2135416	hypothetical protein - human >gi288145	0.012
1172	S61977	medium-chain acyl-CoA dehydrogenase {exon 10, intron 10} [human, Genomic, 1407 nt]	6e-12	113666	!!!! ALU CLASS A WARNING ENTRY !!!!	0.100
1173	X66285	M.musculus DNA for HC1 locus	6e-12	854065	(X83413) U88 [Human herpesvirus 6]	2e-06
1174	S78744	protein S=activated protein C cofactor [rats, liver, mRNA, 3315 nt]	6e-12	2338292	(AF009243) proline-rich Gla protein 2 [Homo sapiens]	3e-10
1175	X58474	Bovine OXT gene for oxytocin, 5' noncoding region	2e-12	1296429	(L77967) small proline-rich protein with paired repeat	4.1
1176	Z56314	H.sapiens CpG DNA, clone 10h10, reverse read cpg10h10.rt1a.	2e-12	2935221	(AF030154) pVII [bovine adenovirus type 3]	2.8
1177	Z56314	H.sapiens CpG DNA, clone 10h10, reverse read cpg10h10.rt1a.	2e-12	2708659	(AF037440) putative 26 kDa protein [Edwardsiella ictaluri]	2.8
1178	Z19543	M.musculus h2-calponin cDNA	2e-12	2497945	BETA SCRUIIN >gi1015535 (Z47541) beta scruiin [Limulus polyphemus]	2e-04

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		erythropoietin				
1179	S45332	receptor [human, placental, Genomic, 8647 nt]	7e-13	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	0.074
1180	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-13	<NONE>	<NONE>	<NONE>
1181	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-13	<NONE>	<NONE>	<NONE>
1182	Z59509	H.sapiens CpG DNA, clone 15a1, reverse read cpg15a1.rt1a.	2e-13	3150251	(AL023634) hypothetical protein	0.66
1183	D10170	Human CYP11B2 gene for steroid 18-hydroxylase	2e-13	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	3e-05
1184	U65416	Human MHC class I molecule (MICB) gene, complete cds	2e-13	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	6e-11
1185	AJ006031	Mus musculus IHABP gene, promoter	8e-14	2132223	hypothetical protein YPL186c - yeast	1.1
1186	U34976	Human gamma-sarcoglycan mRNA, complete cds	8e-14	1054903	(U34976) gamma-sarcoglycan [Homo sapiens] >gi 4239660 sapiens]	0.034
1187	D30647	Rat mRNA for very-long-chain Acyl-CoA dehydrogenase, complete cds	8e-14	3183512	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (VLCAD) >gi 2388724 (AF017176) very-long-chain acyl-CoA dehydrogenase [Mus musculus]	8e-23
1188	Z63247	H.sapiens CpG DNA, clone 7g4, forward read cpg7g4.fl1a.	6e-14	86285	histone H1.01 - chicken	6.8
1189	U27196	Gallus gallus zinc finger protein (Fzf-1) mRNA, complete cds.	3e-14	2134436	zinc finger protein - chicken (fragment)	4e-10
1190	M26219	African green monkey origin of replication	2e-14	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1191	AF100694	Pontin52 mRNA, complete cds	2e-14	4235641	(AF119040) NL0D [Lycopersicon esculentum]	0.65
1192	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-14	3043728	(AB011174) KIAA0602 protein [Homo sapiens]	0.28
1193	AJ005866	Homo sapiens mRNA for putative Sqv-7-like protein, partial	2e-14	4008517	(AJ005866) Sqv-7-like protein [Homo sapiens]	0.004
1194	U32709	Haemophilus influenzae Rd section 24 of 163 of the complete genome	2e-14	3861056	(AJ235272) POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (pnp) [Rickettsia prowazekii]	6e-28
1195	AF073485	Homo sapiens MHC class I-related protein MR1 precursor (MR1) gene, partial cds	8e-15	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1.0
1196	AF052135	Homo sapiens clone 23625 mRNA sequence	8e-15	4098124	(U73522) AMSH [Homo sapiens]	8e-14
1197	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-15	<NONE>	<NONE>	<NONE>
1198	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-15	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	1.7
1199	Z75104	S.cerevisiae chromosome XV reading frame ORF YOR196c	3e-15	3878570	(Z46381) similar to lipoic acid synthase; cDNA EST yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3...	1e-15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1200	X70052	S.cerevisiae sof1 gene	3e-15	1125754	(U42833) coded for by C. elegans cDNA cm16f6; coded for by C. elegans cDNA CEESU63F; similar to S. cerevisiae SOF1 protein (SP:P33750) [Caenorhabditis elegans]	3e-29
1201	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-15	<NONE>	<NONE>	<NONE>
1202	M92295	Gorilla gorilla gamma 1 and gamma-2 globin genes, complete cds.	1e-15	284078	hypothetical protein 2 - human >gi182220	7.4
1203	L34587	Homo sapiens RNA polymerase II elongation factor SIII, p15 subunit mRNA, complete cds. >:: gb AR022286 AR022286 Sequence 7 from patent US 5792634	9e-16	<NONE>	<NONE>	<NONE>
1204	D83649	Xenopus laevis mRNA for xSox7 protein, complete cds	8e-16	2447043	(D83649) xSox7 protein [Xenopus laevis]	4e-06
1205	AC005190	Homo sapiens PAC clone DJ1152D16 from Xq23; complete sequence [Homo sapiens]	3e-16	<NONE>	<NONE>	<NONE>
1206	J03626	Human UMP synthase mRNA, complete cds.	3e-16	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.65
1207	J00083	Human Alu family interspersed repeat; clone BLUR11.	3e-16	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	4e-06
1208	U70674	Mus musculus m-Numb (m-nb) mRNA, complete cds	1e-16	<NONE>	<NONE>	<NONE>

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1209	U66619	Human SWI/SNF complex 60 KDa subunit (BAF60c) mRNA, complete cds	1e-16	1549247	(U66619) SWI/SNF complex 60 KDa subunit [Homo sapiens]	0.003
1210	U75467	Drosophila melanogaster Rga and Atu genes, complete cds	1e-16	1658503	(U75467) Atu [Drosophila melanogaster]	5e-32
1211	M72709	Human alternative splicing factor mRNA, complete cds.	3e-17	<NONE>	<NONE>	<NONE>
1212	U26556	Human ferritin H (FTHL13) pseudogene.	3e-17	<NONE>	<NONE>	<NONE>
1213	D32064	Human gene for 2-oxoglutarate dehydrogenase, complete cds	3e-17	2088843	(AF003386) F59E12.9 gene product [Caenorhabditis elegans]	0.12
1214	M76364	Human (Papua New Guinean) Mitochondrial DNA control region, sequence 131.	3e-17	114009	APAG PROTEIN >gi 72927 pir BVECAG apaG protein - Escherichia coli >gi 40918 (X04711) URF hypothetical protein [Escherichia coli]	0.006
1215	AF017466	Homo sapiens genomic sequence from subtelomeric region of chromosome 4q	1e-17	3947985	(U78948) MADS-box protein 2 [Malus domestica]	4.1
1216	AF004876	Homo sapiens 54Tm (54tm) mRNA, complete cds	1e-17	4101574	(AF004876) 54Tm [Homo sapiens]	0.006
1217	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-18	<NONE>	<NONE>	<NONE>
1218	AF086758	Rattus norvegicus Na-K-2Cl cotransporter	4e-18	3892703	(AL033545) putative glycine-rich protein [Arabidopsis thaliana]	0.30
1219	AF020089	Homo sapiens PEN11B mRNA, complete cds	4e-18	2642493	(AF023910) DNA topoisomerase I [Physarum polycephalum]	0.053
1220	X82333	H.sapiens IRLB gene (exon1-3)	4e-18	106837	irlB protein - human (fragment) >gi 33969	2e-11

HPI

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for KIAA0385 gene, complete cds				
1221	AB002383		4e-18	3228540	(AF060181) zinc finger protein [Homo sapiens]	6e-25
1222	X98485	P.vivax PV14 gene	1e-18	<NONE>	<NONE>	<NONE>
		H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA21E8				
1223	Z79057		1e-18	2981631	(AB012223) ORF2 [Canis familiaris]	0.001
		Homo sapiens (clone JH4B1) PM-scl autoantigen mRNA, complete cds.			nucleolar 100K polymyositis-scleroderma protein - human >gi 35555 (X66113) PM/Scl 100kD nucleolar protein [Homo sapiens]	
1224	L01457		1e-18	346287		0.001
		Dog nonerythroid beta-spectrin mRNA, 3' end.			(AB017037) nonstructural protein precursor [Himetobi P virus]	
1225	L02897		4e-19	3493358		0.12
		Homo sapiens mRNA for APCL protein, complete cds			(AB012162) APCL protein [Homo sapiens]	
1226	AB012162		4e-19	3894265		0.002
		Homo sapiens mRNA for KIAA0521 protein, partial cds			(AB011093) KIAA0521 protein [Homo sapiens]	
1227	AB011093		4e-19	3043566		9e-09
		X.laevis AB21 mRNA for RPD3 homologue			HISTONE DEACETYLASE (HD) thaliana]	
1228	X78454		4e-19	3023945		5e-34
		Human endogenous retrovirus HD1 leader region/integrase-derived ORF1, ORF2, and putative envelope protein mRNA, complete cds			(Z14310) tripartite fusion transcript PLA2L [Human endogenous retrovirus]	
1229	U88895		2e-19	59977		1e-04
		Human tyrosine kinase TXK (txk) gene, exon 13.			!!!! ALU SUBFAMILY J WARNING ENTRY	
1230	U34377		1e-19	728831		3e-05
		M.musculus rab3A gene			(Z99167) putative peroxisomal organisation and biogenesis protein [Schizosaccharomyces pombe]	
1231	X72966		1e-19	2408076		2e-09
		Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484				
1232	AB007953		4e-20	<NONE>	<NONE>	<NONE>

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1233	D14034	Human gene for Zn-alpha2-glycoprotein, complete cds	2e-20	3928756	(AB001535) similar to C.elegans hypothetical protein CET01H8.1,CEC05C12.3,CEF54D1.5. similar to trp and trp-like proteins [Homo sapiens]	1e-07
1234	X82126	H.sapiens HOK-2 gene, exon 2	2e-20	2137269	DNA-binding protein - mouse >gij437444	1e-19
1235	AF093684	Luciferase reporter vector pXP2 *SA, complete sequence	5e-21	2773363	(AF041382) microtubule binding protein D-CLIP-190	5.5
1236	J05272	Human IMP dehydrogenase type 1 mRNA complete cds.	5e-21	124417	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1 (IMP DEHYDROGENASE 1) (IMPDH-I) (IMPD 1) I - human	2e-04
1237	D86997	Human (lambda) DNA for immunoglobulin light chain	5e-21	3878261	(Z75712) Similarity to S. Pombe BEM1/BUD5 suppressor; cDNA EST EMBL:Z14470 comes from this gene; cDNA EST yk482d4.3 comes from this gene; cDNA EST yk482d4.5 comes from this gene [Caenorhabditis elegans]	6e-46
1238	Z79865	H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 302f3, forward read 302f3.f	2e-21	2739037	(AF024614) ADAM 10 [Caenorhabditis elegans] Zinc-binding metalloprotease domain; cDNA EST CEMSA42F comes from this gene; cDNA EST yk218f3.3 comes from this gene; cDNA EST yk443d9.3 comes from this gene; cDNA EST yk443d9.5 comes from this gene; cDNA...	2.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1239	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-22	3924779	(U600563) similar to human B, cDNA EST yk450d8.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from... >gi 3924881 gnl PID e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	0.35
1240	U67824	Human primary Alu transcript	6e-22	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	5e-07
1241	AF070636	Homo sapiens clone 24686 mRNA sequence	2e-22	98710	fatty-acid synthase (EC 2.3.1.85) - Brevibacterium ammoniagenes	2.5
1242	D14034	Human gene for Zn-alpha2-glycoprotein, complete cds	2e-22	4185939	(Y17832) pol protein [Human endogenous retrovirus K]	0.29
1243	M61835	Human lactase phlorizin hydrolase (LCT) gene, exon 2.	2e-22	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.006
1244	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-23	1350828	RABPHILIN-3A >gi 477100 pir A48097 rabphilin-3A - bovine >gi 285646 gnl PID d1003285	0.14
1245	AF074985	Homo sapiens full length insert cDNA YH73H06	8e-24	3170548	(AF056116) unknown [Fugu rubripes]	0.24
1246	D14878	Human mRNA for protein D123, complete cds	7e-24	<NONE>	<NONE>	<NONE>
1247	D16917	Human HepG2 3' region cDNA, clone hmd3d07	6e-24	1397345	(U61955) contains multiple region of strong similarity to C2H2-type zinc fingers (PS:PS00028) [Caenorhabditis elegans]	2.4

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1248	Z69654	sequence from cosmid L98A6, Huntington's Disease Region, chromosome 4p16.3.	3e-24	4240566	(AF123462) neurexin III (Homo sapiens)	4.5
1249	AB007914	Homo sapiens mRNA for KIAA0445 protein, complete cds	2e-24	3885949	(AF095568) amelogenin (Paleosuchus palpebrosus)	3.2
1250	AF088072	Homo sapiens full length insert cDNA clone ZD93D10	2e-24	323091	immunodominant microneme protein Etp100 - Eimeria tenella >gi 2707733 (AF032905) microneme protein precursor Etmic-1 (Eimeria tenella)	0.34
1251	AF069489	Homo sapiens cAMP specific phosphodiesterase 4A variant pde46 (PDE4A) gene, exons 2 through 13 and alternative splice exons 3a, 6a, 6b, and 9a	2e-24	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	1e-05
1252	Y12853	Homo sapiens P2X7 gene, exon 4-8	9e-25	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-05
1253	M27830	Human 28S ribosomal RNA gene, complete cds.	8e-25	<NONE>	<NONE>	<NONE>
1254	AB007953	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484	8e-25	<NONE>	<NONE>	<NONE>
1255	Z60212	H.sapiens CpG DNA, clone 195c8, forward read cpg195c8.ft1a.	8e-25	158154	(M81959) POU domain protein [Drosophila melanogaster]	3.3
1256	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-25	<NONE>	<NONE>	<NONE>
1257	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-25	<NONE>	<NONE>	<NONE>
1258	Y12851	Homo sapiens P2X7 gene, exon 1 and joined CDS	2e-25	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus Tera				
1259	U64033	(Tera) mRNA, complete cds	9e-26	<NONE>	<NONE>	<NONE>
1260	U19181	Rattus norvegicus Rabin3 mRNA, complete cds.	9e-26	624225	(U19181) Rabin3 [Rattus norvegicus]	1e-13
1261	AF020788	Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds	9e-26	3915881	SEL-10 PROTEIN Candida CDC4 gene (TR:E234056); cDNA EST EMBL:D27699 comes from this gene; cDNA EST EMBL:D27698 comes from this gene; cDNA EST EMBL:D32793 comes from this gene; cDNA EST EMBL:D33271 comes from this gen...	7e-32
1262	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	8e-26	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	0.045
1263	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-26	3878629	(Z93385) predicted using Genefinder; Similarity to B.subtilis GTP-binding protein	2e-10
1264	X91195	H.sapiens SOM172 mRNA	1e-26	<NONE>	<NONE>	<NONE>
1265	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-26	1360637	(X95995) ENBP1 [Vicia sativa]	3.1
1266	L08237	Human MG21 mRNA, partial cds.	1e-26	950411	(L08237) located at OATL1 [Homo sapiens]	9e-09
1267	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-27	3881080	(AL032657) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h6.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk467g8,....	0.001
1268	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-27	1731324	HYPOTHETICAL PROTEIN >gil166306	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1269	X89211	H.sapiens DNA for endogenous retroviral like element	8e-27	2065209	(Y12713) Gag polyprotein [Mus musculus]	0.005
1270	U73166	Homo sapiens cosmid clone LUCA15 from 3p21.3, complete sequence [Homo sapiens]	3e-27	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	4e-04
1271	D78255	Mouse mRNA for PAP-1, complete cds	3e-27	1850098	(D78255) PAP-1 [Mus musculus]	2e-10
1272	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.39
1273	AB015202	Homo sapiens gene for hippocalcin, exon 2, 3 and complete cds	1e-27	3877698	(Z83318) predicted using Genefinder; cDNA EST yk369e7.5 comes from this gene [Caenorhabditis elegans]	0.37
1274	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3328188	(AF074902) laminin alpha chain [Caenorhabditis elegans]	0.19
1275	Z29336	H.sapiens gene for Cu/Zn-superoxide dismutase	1e-27	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	6e-05
1276	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	9.2
1277	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.054
1278	AB001636	Homo sapiens mRNA for ATP-dependent RNA helicase #46, complete cds	4e-28	3913425	POTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi 2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana] (AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	3e-22
1279	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-28	4056454		0.066

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1280	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-05
1281	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1282	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1283	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1284	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1285	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1286	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1287	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	140505	PROBABLE INTRON MATURASE liverwort (Marchantia polymorpha) chloroplast >gi 11663	3.0
1288	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	140505	PROBABLE INTRON MATURASE liverwort (Marchantia polymorpha) chloroplast >gi 11663	1.8
1289	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.50
1290	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.087
1291	Z63029	H.sapiens CpG DNA, clone 77b3, forward read cpg77b3.ft1a.	1e-28	2493240	HYPOTHETICAL 29.3 KD PROTEIN pseudotsugata nuclear polyhedrosis virus]	0.014

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1292	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.010
1293	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.007
1294	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1295	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	126363	LAMININ ALPHA-1 CHAIN PRECURSOR precursor - human	3e-04
1296	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-04
1297	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	3e-05
1298	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3157926	(AC002131) Strong similarity to extensin-like protein gb Z34465 from Zea mays. [Arabidopsis thaliana]	2e-05
1299	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1300	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	320919	kinetoplast-associated protein - Trypanosoma cruzi >gi 162142 (M25364) kinetoplast-associated protein	1e-07
1301	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-08
1302	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-09
1303	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-10
1304	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-10
1305	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-11
1306	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-11

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1307	AF100694	Pontin52 mRNA, complete cds	4e-29	<NONE>	<NONE>	<NONE>
1308	AF079529	Homo sapiens cAMP-specific phosphodiesterase 8B	4e-29	<NONE>	<NONE>	<NONE>
1309	X93334	H.sapiens mitochondrial DNA, complete genome	4e-29	116977	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - human mitochondrion (SGC1) >gi 13006 (V00662) cytochrome oxidase I [Homo sapiens] >gi 506829 (J01415) cytochrome oxidase subunit 1 [Homo sapiens] sapiens]	3e-09
1310	AF020760	Homo sapiens serine protease (Omi) mRNA, complete cds	4e-29	2738915	(AF020760) serine protease [Homo sapiens]	8e-12
1311	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	4e-29	2072294	(U95097) mitotic phosphoprotein 43 [Xenopus laevis]	1e-25
1312	L32162	Homo sapiens transcription factor mRNA, 5' end.	2e-29	2501706	RENAL TRANSCRIPTION FACTOR KID-1 finger protein [Mus musculus]	8e-15
1313	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-29	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-04
1314	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-29	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	1e-05
1315	U50839	Homo sapiens g16 protein (g16) mRNA, complete cds	1e-29	3212101	(AF069517) RNA binding protein DEF-3 [Homo sapiens]	6e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					intercellular adhesion molecule	
1316	X69711	H. sapiens mRNA for ICAM-R	5e-30	299356	3, ICAM-3=lymphocyte function-associated antigen 1 counter-receptor homolog [human, tonsil, Peptide Partial, 518 aa]	3e-08
1317	AF010227	Homo sapiens receptor-associated coactivator 3	5e-30	2331250	(AF012108) Amplified in Breast Cancer [Homo sapiens]	8e-09
1318	AF086395	Homo sapiens full length insert cDNA clone ZD75C01	2e-30	3861241	(AJ235273) CELL SURFACE ANTIGEN (sca5)	4.2
1319	M27830	Human 28S ribosomal RNA gene, complete cds.	2e-30	1730522	PHOSPHOGLYCERATE KINASE 2.7.2.3 - Pyrococcus woesei >gi 1054832 (X73527) phosphoglycerate kinase [Pyrococcus woesei]	3.8
1320	M79307	Mouse GTP-binding protein (Rab17) mRNA sequence.	2e-30	464564	RAS-RELATED PROTEIN RAB-17 Rab17 - mouse (fragment) >gi 297157 (X70804) rab17 [Mus musculus]	9e-11
1321	AL022168	Human DNA sequence from clone U247E12 on chromosome Xq22-23, complete sequence [Homo sapiens]	1e-30	2072967	(U93570) putative p150 [Homo sapiens]	3e-11
1322	X85124	M.musculus pacsin gene	1e-30	2217964	(Z50798) p52 [Gallus gallus]	1e-34
1323	U37408	Homo sapiens phosphoprotein CtBP mRNA, complete cds	5e-31	74518	structural polyprotein - Venezuelan equine encephalitis virus (strain TRD) >gi 323710. (J04332) poly-envelope protein [Venezuelan equine encephalitis virus]	1.1
1324	L04193	Human lens membrane protein (mp19) gene, exon 11.	2e-31	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	7e-07
1325	M11167	Human 28S ribosomal RNA gene.	6e-32	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1326	M33336	Human cAMP-dependent protein kinase type I-alpha subunit (PRKAR1A) mRNA, complete cds	2e-32	<NONE>	<NONE>	<NONE>
1327	J03060	Human glucocerebrosidase pseudogene, complete cds	2e-32	2144479	glucosylceramidase (EC 3.2.1.45) precursor - human	1e-05
1328	U33053	Human lipid-activated protein kinase PRK1 mRNA, complete cds	7e-33	2137689	protein kinase (EC 2.7.1.37) - mouse	1e-14
1329	J04617	Human elongation factor EF-1-alpha gene, complete cds. > :: dbj E02629 E02629 DNA of human polypeptide chain elongation factor-1 alpha	6e-33	<NONE>	<NONE>	<NONE>
1330	L40396	Homo sapiens (clone s22i71) mRNA fragment	6e-33	124235	INTERMEDIATE FILAMENT PROTEIN B protein B - common roundworm	1.00
1331	Z72813	S.cerevisiae chromosome VII reading frame ORF YGR028w	6e-33	1709135	MSP1 PROTEIN HOMOLOG Yeast MSP1 protein (TAT-binding homolog 4)	8e-50
1332	AB007941	Homo sapiens mRNA for KIAA0472 protein, partial cds	2e-33	1150834	(U42471) Wiscott-Aldrich Syndrome protein homolog [Mus musculus]	2.0
1333	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	2e-34	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	6e-15
1334	D14657	Human mRNA for KIAA0101 gene, complete cds	7e-35	<NONE>	<NONE>	<NONE>
1335	X69910	H.sapiens p63 mRNA for transmembrane protein	7e-35	2136323	trithorax homolog HTX - human (fragment) homolog=MLL (alternative splicing, clone 14p-18B)	0.94

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1336	AF053455	tetraspan TM4SF (TSPAN-5) gene, complete cds	7e-35	3152703	(AF065389) tetraspan NET-4 [Homo sapiens]	1e-25
1337	X58374	D.melanogaster crm mRNA	3e-35	117478	CROOKED NECK PROTEIN	6e-41
1338	AF086492	Homo sapiens full length insert cDNA clone ZD95D11	9e-36	2909809	(AF031328) aminoglycoside 6'-N-acetyltransferase It	1.9
1339	Z96223	H.sapiens telomeric DNA sequence, clone 12PTEL120, read 12PTELOO120.seq	3e-36	2408068	(Z99165) hypothetical protein	0.61
1340	Z37986	H.sapiens mRNA for phenylalkylamine binding protein.	1e-36	1362793	emopamil-binding protein - human >gi 780263	5e-11
1341	U57847	Human ribosomal protein S27 mRNA, complete cds. end similar to similar to metallopanstimulin 1 >:: gb AA316327 AA316327 EST188061 HCC cell line (matatasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to metallopanstimulin 1	3e-37	1171014	40S RIBOSOMAL PROTEIN S27 growth factor-inducible zinc finger protein MPS-1 - human >gi 431319 (L19739) metallopanstimulin [Homo sapiens] >gi 1373421 (U57847) ribosomal protein S27	1.4
1342	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial	3e-37	3123027	70 KD WD-REPEAT TUMOR-SPECIFIC ANTIGEN >gi 2505957 gnl PID c353992 (Y15054) 70 kD tumor-specific antigen [Rattus norvegicus]	2e-15
1343	AF084205	Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds	3e-37	3452473	(AF084205) serine/threonine protein kinase TAO1 [Rattus norvegicus]	5e-4
1344	X78604	R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5	1e-37	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1345	AJ236644	Homo sapiens chromosome 22 CpG island DNA, genomic MseI fragment, clone 22CGIB49A3, complete read	1e-37	2239219	(Z97210) hypothetical protein	6e-05
1346	U09367	Human zinc finger protein ZNF136	4e-39	2137269	DNA-binding protein - mouse >gi437444	7e-23
1347	Z69649	Human DNA sequence from cosmid L69F7B, Huntington's Disease Region, chromosome 4p16.3 contains Huntington Disease (HD) gene.	3e-39	3096918	(AL023094) putative cyclase associated protein CAP [Arabidopsis thaliana]	5.6
1348	AF065389	Homo sapiens tetraspan NET-4 mRNA, complete cds	1e-39	3152703	(AF065389) tetraspan NET-4 [Homo sapiens]	6e-29
1349	AF038172	Homo sapiens clone 23923 mRNA sequence	1e-40	1813464	(U60883) CapC [Bacillus firmus]	2.8
1350	Z83095	H.sapiens Fanconi anaemia group A gene, exons 39, 40, 41, 42 and 43	1e-40	2137870	zinc finger protein - mouse (fragment)	3e-23
1351	AF057734	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 16	1e-40	2842416	(AL008730) dJ487J7.1.1 (putative protein dJ487J7.1 isoform 1) [Homo sapiens]	6e-61
1352	AF070567	Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds	4e-41	3133087	(Y15718) dystrobrevin B DTN-B2 [Homo sapiens]	7e-13
1353	AF006088	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16) mRNA, complete cds	2e-41	3121767	ARP2/3 COMPLEX 16 KD SUBUNIT	3e-36
1354	X69942	M.musculus mRNA of enhancer-trap-locus 1	6e-42	2291152	(AF016418) No definition line found [Caenorhabditis elegans]	6.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1355	X87838	H.sapiens mRNA for beta-catenin	5e-42	1373019	(U28811) cysteine-rich fibroblast growth factor receptor	8e-05
1356	AB018268	Homo sapiens mRNA for KIAA0725 protein, partial cds	5e-42	3882171	(AB018268) KIAA0725 protein [Homo sapiens]	2e-33
1357	M84424	Human cathepsin E (CTSE) gene, exon 9 and complete cds.	2e-42	<NONE>	<NONE>	<NONE>
1358	U80776	Human EST clone NIB1543 mariner transposon Hsmar1 orf gene, complete cds	2e-42	2231380	(U80776) orf; encodes putative chimeric protein with SET domain in N-terminus with similarity to several other human, Drosophila, nematode and yeast proteins [Homo sapiens]	3e-11
1359	U55184	Human G protein Golf alpha gene, exon 12 and complete cds	2e-42	3165531	(AF067608) No definition line found [Caenorhabditis elegans]	1e-16
1360	AC005190	Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence [Homo sapiens]	6e-43	2978255	(AB007407) myeloid zinc finger protein-2 [Mus musculus]	2.3
1361	AB018284	Homo sapiens mRNA for KIAA0741 protein, complete cds	5e-43	<NONE>	<NONE>	<NONE>
1362	AB011137	Homo sapiens mRNA for KIAA0565 protein, complete cds	5e-43	3043654	(AB011137) KIAA0565 protein [Homo sapiens]	1e-07
1363	M93651	Human set gene, complete cds.	2e-43	<NONE>	<NONE>	<NONE>
1364	Z47087	H.sapiens mRNA for RNA polymerase II elongation factor-like protein.	2e-43	1872514	(U84404) E6-associated protein E6-AP/ubiquitin-protein ligase [Homo sapiens] >gi 2361031 (AF016708) E6-AP ubiquitin-protein ligase [Homo sapiens]	7.2
1365	U27197	Drosophila melanogaster pelota (pelo) mRNA, complete cds	2e-43	1352736	PELOTA PROTEIN >gi 973224 (U27197) pelota [Drosophila melanogaster]	1e-46

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1366	D80007	Human mRNA for KIAA0185 gene, partial cds	6e-44	2498864	RRP5 PROTEIN HOMOLOG (KIAA0185) hypothetical protein YM9959.11C of <i>S.cerevisiae</i> . [Homo sapiens]	6e-09
1367	AF005039	Homo sapiens secretory carrier membrane protein (SCAMP3) mRNA, complete cds	6e-44	2232243	(AF005039) secretory carrier membrane protein [Homo sapiens]	2e-09
1368	X68101	<i>R.norvegicus</i> trg mRNA	2e-44	550420	(X68101) trg gene product [<i>Rattus norvegicus</i>]	1e-37
1369	AF044206	Homo sapiens cyclooxygenase (COX-2) gene, promoter and exon 1	2e-45	2072953	(U93565) putative p150 [Homo sapiens]	5e-06
1370	L48708	Homo sapiens faciogenital dysplasia (FGD1) gene, 5' end of intron 17	8e-46	<NONE>	<NONE>	<NONE>
1371	X15822	Human COX VIIa-L mRNA for liver-specific cytochrome c oxidase (EC 1.9.3.1.)	3e-46	117121	CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR >gi 2144370 pir OSHU7L cytochrome-c oxidase (EC 1.9.3.1) chain VIIa precursor, hepatic - human >gi 30147 (X15822) precursor (AA -23 to 60) [Homo sapiens]	5e-13
1372	U47323	Mus musculus stromal cell protein mRNA, complete cds	3e-46	1493833	(U47323) stromal cell protein [Mus musculus]	1e-48
1373	AF059524	Homo sapiens reticulon gene family protein	7e-47	1731169	HYPOTHETICAL 113.1 KD PROTEIN T28D9.7 IN CHROMOSOME II >gi 861264 (U28738) coded for by <i>C. elegans</i> cDNA yk8h5.3; coded for by <i>C. elegans</i> cDNA yk8h5.5; similar to <i>C. elegans</i> deg-1 and mec-4 in exon 2 [<i>Caenorhabditis elegans</i>]	7.8
1374	AJ132583	Homo sapiens mRNA for puromycin sensitive aminopeptidase, partial	3e-47	1777519	(U39123) T cell receptor beta chain [Homo sapiens]	9.7

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1375	M97856	Homo sapiens histone binding protein mRNA, complete cds.	3e-47	2645327	(U83821) NADH dehydrogenase subunit 3 [Oryzomys palustris]	5.7
1376	U53220	Human retinoblastoma-related Rb2/p130 gene, 5' flanking region and partial cds	3e-47	2499225	CMP-SIALIC ACID TRANSPORTER CMP-sialic acid transporter [Cricetulus griseus]	5.3
1377	X87870	H.sapiens mRNA for hepatocyte nuclear factor 4a	1e-47	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	7.3
1378	AF060195	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds	3e-48	478681	limb deformity protein - chicken	0.25
1379	AB018285	Homo sapiens mRNA for KIAA0742 protein, partial cds	1e-48	3122969	TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA) >gi 281040 pir S28499 probable zinc finger protein - rat >gi 57504 (X59993) zinc finger protein	1e-30
1380	U35032	Human endogenous retrovirus clone c5.11, HERV-H multiply spliced subgenomic leader, protease and integrase region mRNA, partial cds	4e-49	88558	retroviral proteinase-like protein - human	6e-05
1381	AB007956	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487	1e-49	<NONE>	<NONE>	<NONE>
1382	D86987	Homo sapiens mRNA for KIAA0214 protein, complete cds	1e-49	2497944	ALPHA SCRUIIN >gi 633238 (Z38132) scruiin [Limulus polyphemus] >gi 1093326 prf 2103269A scrulin [Limulus sp.]	9.7
1383	U25826	Human transcription factor (SC1) gene, complete cds.	4e-50	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus ATP-dependent RNA helicase mRNA, partial cds.				
1384	U46690		4e-50	1335873	(U46690) ATP-dependent RNA helicase [Mus musculus]	3e-24
1385	AF072128	Mus musculus claudin-2 mRNA, complete cds	2e-50	3335184	(AF072128) claudin-2 [Mus musculus]	4e-24
1386	AF093593	Homo sapiens snRNA activating protein complex 19kDa subunit (SNAP19) mRNA, complete cds	1e-50	3668416	(AF093593) snRNA activating protein complex 19kDa subunit [Homo sapiens]	0.003
1387	U79745	Homo sapiens monocarboxylate transporter homologue MCT6 mRNA, complete cds	1e-50	1177607	(X92485) pva1 [Plasmodium vivax]	2e-07
1388	L09647	Rattus norvegicus hepatocyte nuclear factor 3a	1e-50	404764	(L10409) fork head related protein [Mus musculus]	2e-21
1389	X61506	Mouse E46 mRNA for E46 protein	4e-51	114909	BRAIN PROTEIN E46	1e-20
1390	M33387	Human debrisoquine 4-hydroxylase (CYP2D8P) and	1e-51	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	5e-15
1391	AF019767	Homo sapiens zinc finger protein (ZPR1) mRNA, complete cds	4e-52	961507	(D63788) anchor protein, LCM	5.9
1392	Z37986	H.sapiens mRNA for phenylalkylamine binding protein.	2e-52	<NONE>	<NONE>	<NONE>
1393	U65416	Human MHC class I molecule (MICB) gene, complete cds	2e-52	3878637	(Z49128) weak similarity with SINR protein (Swiss Prot accession number P06533); cDNA EST EMBL:T00631 comes from this gene; cDNA EST yk293d10.5 comes from this gene [Caenorhabditis elegans]	8.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1394	Z57647	H.sapiens CpG DNA, clone 189a6, forward read cpg189a6.ft1a.	2e-52	111187	beta-globin DNA-binding protein B1, transcription factor PU.1 - mouse >gi 200586 (M32370) PU.1 protein [Mus musculus] >gi 200972 (M38252) transcription factor Pu.1 [Mus musculus]	5.8
1395	L13738	Human activated p21cdc42Hs kinase (ack) mRNA, complete cds.	2e-52	2921447	(AF037260) non-receptor protein tyrosine kinase Ack [Mus musculus]	7e-23
1396	AF042379	Homo sapiens spindle pole body protein spe97 homolog GCP2 mRNA, complete cds	7e-53	2801701	(AF042379) spindle pole body protein spe97 homolog GCP2	1e-16
1397	AF047441	Homo sapiens RNA polymerase I 40kD subunit mRNA, complete cds	6e-53	3914807	DNA-DIRECTED RNA POLYMERASE I 40 KD POLYPEPTIDE (RPA40) (RPA39) >gi 2266929 (AF008442) RNA polymerase I subunit hRPA39 [Homo sapiens]	4e-19
1398	AF104670	Homo sapiens cell cycle protein (PA2G4) gene, exons 6 through 13, and complete cds	2e-53	<NONE>	<NONE>	<NONE>
1399	S60754	{ VNTR locus DXZ4, hypervariable tandem repeat cluster } [human, Genomic, 2991 nt] > :: gb L07935 HUMVNT RA Homo sapiens microsatellite VNTR DNA sequence.	2e-53	1209669	(U38810) CAGR1 [Homo sapiens] >gi 3098420 (AF040945) homeotic regulator homolog MAB21 [Mus musculus]	4.6
1400	D86972	Human mRNA for KIAA0218 gene, complete cds	1e-53	3426041	(AC005168) unknown protein [Arabidopsis thaliana]	9.1

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1401	AJ236682	Homo sapiens chromosome 22 CpG island DNA, genomic MseI fragment, clone 22CGIB49E6, complete read	7e-54	3928721	(AL034355) putative cytochrome oxidase subunit I [Streptomyces coelicolor]	0.30
1402	AJ236682	Homo sapiens chromosome 22 CpG island DNA, genomic MseI fragment, clone 22CGIB49E6, complete read	6e-54	3928721	(AL034355) putative cytochrome oxidase subunit I [Streptomyces coelicolor]	0.28
1403	M37583	Human histone (H2A.Z) mRNA, complete cds.	6e-54	70711	histone H2A.F, embryonic - chicken	2e-16
1404	AJ009947	Homo sapiens mRNA for putative ATPase, partial	6e-54	3550295	(AJ009947) putative ATPase [Homo sapiens]	3e-18
1405	Y08459	B.taurus mRNA for novel cytoplasmic protein	2e-54	<NONE>	<NONE>	<NONE>
1406	AF042384	Homo sapiens BC-2 protein mRNA, complete cds	2e-54	2828147	(AF042384) BC-2 protein [Homo sapiens]	2e-14
1407	AF042379	Homo sapiens spindle pole body protein spc97 homolog GCP2 mRNA, complete cds	8e-55	2801701	(AF042379) spindle pole body protein spc97 homolog GCP2	2e-17
1408	AF005355	Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds	7e-55	3253159	(AF005355) translation initiation factor eIF2C	3e-53
1409	AF008442	Homo sapiens RNA polymerase I subunit hRPA39 mRNA, complete cds	3e-55	3335138	(AF047441) RNA polymerase I 40kD subunit [Homo sapiens]	3e-20
1410	AF047441	Homo sapiens RNA polymerase I 40kD subunit mRNA, complete cds	3e-55	3335138	(AF047441) RNA polymerase I 40kD subunit [Homo sapiens]	3e-20

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for				
1411	X08004	Rap1B protein > :: emb A08693 A08693 H.sapiens rap1b cDNA	2e-55	539995	transforming protein rap1b - rat (strain Copenhagen)	2e-18
1412	AF010403	Homo sapiens ALR mRNA, complete cds	2e-55	2358285	(AF010403) ALR [Homo sapiens]	1e-49
1413	M77016	Human tropomodulin mRNA, complete cds.	8e-56	262249	(S52010) orf1 5' of EpoR [mice, Peptide, 85 aa] [Mus sp.]	0.027
1414	AB020633	Homo sapiens mRNA for KIAA0826 protein, partial cds	2e-56	<NONE>	<NONE>	<NONE>
1415	X87489	H.sapiens genomic DNA (chromosome 3; clone NL1243D)	2e-56	1814029	(U84501) cuticle collagen [Caenorhabditis briggsae]	0.038
1416	AB007893	Homo sapiens KIAA0433 mRNA, partial cds	2e-56	2887437	(AB007893) KIAA0433 [Homo sapiens]	9e-21
1417	X78925	H.sapiens HZF2 mRNA for zinc finger protein	1e-56	3342002	(AF054180) hematopoietic cell derived zinc finger protein [Homo sapiens]	2e-21
1418	Z56281	H.sapiens mRNA for interferon regulatory factor 3	9e-57	2497442	INTERFERON REGULATORY FACTOR 3 factor 3 [Homo sapiens]	2e-21
1419	U78772	Homo sapiens nuclear VCP-like protein NVLp.1	8e-57	2406565	(U68140) nuclear VCP-like protein NVLp.2 [Homo sapiens]	5e-20
1420	D79994	Human mRNA for KIAA0172 gene, partial cds	3e-57	1136404	(D79994) similar to ankyrin of Chromatium vinosum. [Homo sapiens]	9e-38
1421	AB002342	Human mRNA for KIAA0344 gene, complete cds	1e-57	2224629	(AB002342) KIAA0344 [Homo sapiens]	4e-20
1422	L19437	Human transaldolase mRNA containing transposable element, complete cds	1e-57	1553119	(U63159) transaldolase [Mus musculus]	2e-20
1423	D17532	Human mRNA for RCK, complete cds	9e-58	129376	PROBABLE ATP- DEPENDENT RNA HELICASE P54 (ONCOGENE RCK) (DEAD BOX PROTEIN 6)	1e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1424	X79568	H.sapiens BDPI mRNA for protein-tyrosine-phosphatase	9e-58	1871531	(X79568) protein-tyrosine-phosphatase	1e-22
1425	X79568	H.sapiens BDPI mRNA for protein-tyrosine-phosphatase	9e-58	1871531	(X79568) protein-tyrosine-phosphatase	9e-23
1426	AB012295	Homo sapiens HKE1.5 mRNA for GDS-related protein, complete cds	7e-58	2648021	(Z97184) RGL2 [Homo sapiens]	9e-19
1427	AF086040	Homo sapiens full length insert cDNA clone YX52E07	1e-58	543222	glutamine (Q)-rich factor 1, QRF-1 - mouse factor 1, QRF-1 [mice, B-cell leukemia, BCL1, Peptide Partial, 84 aa]	3e-36
1428	AB018195	Homo sapiens ca xi mRNA for carbonic anhydrase-related protein XI, complete cds	4e-59	<NONE>	<NONE>	<NONE>
1429	AF071777	Mus musculus IRE1 (Ire1) mRNA, complete cds	4e-59	3766209	(AF071777) IRE1 [Mus musculus]	7e-28
1430	AB000462	Homo sapiens mRNA for SH3 binding protein, complete cds, clone:RES4-23A	3e-59	<NONE>	<NONE>	<NONE>
1431	AF038172	Homo sapiens clone 23923 mRNA sequence	3e-59	3758855	(Z98551) MAL3P6.11 [Plasmodium falciparum]	1.3
1432	Z84812	Human DNA sequence from phage pTEL from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs	1e-59	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	2.5
1433	U36484	Human laminin-binding protein gene, partial cds, and E2 small nucleolar RNA gene, complete sequence	1e-59	226005	protein 40kD [Mus musculus]	7e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					DUAL SPECIFICITY	
1434	L11285	Homo sapiens ERK activator kinase (MEK2) mRNA.	1e-59	2499630	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 (MAP KINASE KINASE 2) (MAPKK 2) kinase type 2 [Gallus gallus]	3e-21
1435	AF086555	Homo sapiens full length insert cDNA clone ZE14E04	4e-60	3287674	(AC005239) F23149_1 [Homo sapiens]	2e-04
1436	M24766	Human (clone pHAIV2-12) alpha-2 collagen type IV	4e-60	29551	(X05610) alpha (2) chain [Homo sapiens]	6e-15
1437	X65550	H. sapiens mki67a mRNA (long type) for antigen of monoclonal antibody Ki-67	4e-60	1170654	ANTIGEN KI-67 >gi 539555 pir A48666 cell proliferation antigen Ki-67, long form - human Ki-67 [Homo sapiens]	3e-15
1438	M27319	Human calmodulin mRNA, complete cds.	4e-60	1345451	(X05949) Calmodulin (AA 2 - 59) (449 is 1st base in codon) [Drosophila melanogaster]	7e-20
1439	Y12781	Homo sapiens mRNA for transducin (beta) like 1 protein	3e-60	62133	(X06172) put. 134 kD protein (AA 1 - 1187); put. replicase	7.4
1440	AB002383	Human mRNA for KIAA0385 gene, complete cds	1e-60	1001548	(D64000) hypothetical protein	4.4
1441	AF070614	Homo sapiens clone 24732 unknown mRNA, partial cds	2e-61	3283879	(AF070614) unknown [Homo sapiens]	3e-17
1442	AB002326	Human mRNA for KIAA0328 gene, partial cds	6e-62	547891	MICROTUBULE-ASSOCIATED PROTEIN 4 microtubule-associated protein-U [Bos taurus]	5.6
1443	AF086471	Homo sapiens full length insert cDNA clone ZD88A01	5e-62	<NONE>	<NONE>	<NONE>
1444	AB002311	Human mRNA for KIAA0313 gene, complete cds	2e-62	2506357	2,3-DIHYDROXYPHENYLPROPIONATE 1,2-DIOXYGENASE >gi 1657544 (U73857) similar to mcp1 gene (catechol 2,3-dioxygenase) of A. eutrophus 3-(2,3-dihydroxyphenylpropionate)1, 2-dioxygenase 2,3-dihydroxyphenylpropionate 1,2-dioxygenase	3.4

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1445	AF069737	Xenopus laevis notchless (nle) mRNA, complete cds	2e-62	3687833	(AF069737) notchless [Xenopus laevis]	1e-55
1446	AF044209	Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds	5e-63	2137603	nuclear receptor co-repressor N-CoR - mouse musculus] >gi1583865 prf 2121436A thyroid hormone receptor co-repressor [Mus musculus]	2e-47
1447	M69238	Human aryl hydrocarbon receptor nuclear translocator (ARNT) mRNA, complete cds.	2e-63	2702319	(AF001307) aryl hydrocarbon receptor nuclear translocator; Arnt [Homo sapiens]	5e-19
1448	X80497	H.sapiens PHKLA mRNA	2e-63	1170685	PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, LIVER ISOFORM (PHOSPHORYLASE KINASE ALPHA L SUBUNIT) >gi1663010 (X80497) phosphorylase kinase phosphorylase kinase alpha subunit [Homo sapiens]	5e-22
1449	AF031141	Homo sapiens ubiquitin conjugating enzyme	2e-63	2623260	(AF031141) ubiquitin conjugating enzyme [Homo sapiens]	1e-23
1450	Z37166	H.sapiens BAT1 mRNA for nuclear RNA helicase	6e-64	2500529	PROBABLE ATP-DEPENDENT RNA HELICASE P47 >gi2135840 pir 137201 nuclear RNA helicase (DEAD family) BAT1 - human >gi587146 (Z37166) nuclear RNA helicase (DEAD family) [Homo sapiens]	9e-24
1451	M64240	Human helix-loop-helix zipper protein (max) mRNA, complete cds. > :: gb 41138 41138 Sequence 1 from patent US 5624818 > :: gb 177062 177062 Sequence 1 from patent US 5693487	5e-64	88175	Myc-binding factor Max, short form - human	8e-22

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1452	M98252	Homo sapiens lysyl hydroxylase (partial clone 2.2 Kb LH) RNA, complete mature peptide.	2e-64	400205	PROCOLLAGEN-LYSINE 3-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (LYSYL HYDROXYLASE) lysyl hydroxylase [Homo sapiens]	7e-22
1453	U09550	Human oviductal glycoprotein mRNA, complete cds.	8e-65	2493676	OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN)	2e-11
1454	X67877	R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein	7e-65	423664	resiniferatoxin-binding protein RBP-26, cytosolic - rat >gi 311660 (X67877) cytosolic resiniferatoxin binding protein RBP-26 [Rattus norvegicus] >gi 1093373 prf 2103310A resiniferatoxin-binding protein [Rattus norvegicus]	2e-40
1455	AB018254	Homo sapiens mRNA for KIAA0711 protein, complete cds	6e-65	92298	glutamine/glutamic acid-rich protein	0.98
1456	J03607	Human 40-kDa keratin intermediate filament precursor gene.	3e-65	1070608	keratin 19, type I, cytoskeletal - human sapiens]	4e-07
1457	U65896	Human gamma-glutamyl carboxylase gene, complete cds	2e-65	<NONE>	<NONE>	<NONE>
1458	U07681	Human NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor mRNA, complete cds.	2e-65	1708399	ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) dehydrogenase alpha chain precursor - human >gi 706839 subunit precursor [Homo sapiens]	4e-26
1459	U88080	Human zinc finger protein (LD5-1) gene, exons 4, 5 and 6, and complete cds	2e-65	1373394	(U57796) zinc finger protein [Homo sapiens] >gi 2306773	2e-39

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1460	M96625	Gallus domesticus tensin mRNA sequence.	3e-66	2134419	tensin - chicken (fragment) >gi 63805 (Z18529) tensin [Gallus gallus] >gi 212755 (L06662) tensin [Gallus gallus]	1e-51
1461	U13262	Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.	1e-70	536926	(U13262) myelin gene expression factor [Mus musculus]	9e-42
1462	U64033	Mus musculus Tera (Tera) mRNA, complete cds	5e-72	1575505	(U64033) Tera [Mus musculus]	9e-34
1463	X78989	M.musculus mRNA for testin	6e-74	1351218	TESTIN 2 (TES2) [CONTAINS: TESTIN 1]	8e-31
1464	U64033	Mus musculus Tera (Tera) mRNA, complete cds	2e-74	1575505	(U64033) Tera [Mus musculus]	5e-37
1465	AF057365	Canis familiaris UDP N-acetylglucosamine transporter mRNA, complete cds	9e-79	3298605	(AF057365) UDP N-acetylglucosamine transporter [Canis familiaris]	9e-10
1466	AJ006064	Rattus norvegicus mRNA for coronin-like protein	1e-82	3757680	(AJ006064) coronin-like protein [Rattus norvegicus]	3e-62
1467	U91582	Macaca fascicularis UDP-glucuronosyltransferase mRNA, complete cds	4e-89	140396	KARYOGAMY PROTEIN KAR4 yeast (Saccharomyces cerevisiae)	1e-08
1468	X06762	Mouse Hox2.3 mRNA	3e-92	123255	HOMEODOMAIN PROTEIN HOXB7 (HOX-2C)	9e-23
1469	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	5e-94	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	7e-34
1470	X74504	M.musculus T10 mRNA	7e-97	1711658	SER/THR-RICH PROTEIN T10 IN DCCR REGION >gi 480900 pir S37488 gene T10 protein - mouse	3e-59

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1471	U13175	Rattus norvegicus clone ubc10a ubiquitin conjugating enzyme (E217kB) mRNA, complete cds.	3e-98	1351345	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 3) >gi 1085588 pir S53358 ubiquitin conjugating enzyme (E217kB) - rat >gi 595666 (U13175) ubiquitin conjugating enzyme [Rattus norvegicus] >gi 1145691 (U39318) UbcH5C [Homo sapiens]	5e-05
1472	S79873	h-lamp-2=lysosome-associated membrane protein-2 protein-2b (LAMP2) mRNA, alternatively spliced form h-lamp-2b, complete cds.	e-119	<NONE>	<NONE>	<NONE>
1473	D13623	Rat mRNA for p34 protein, complete cds	e-112	480379	ribosome-binding protein p34 - [rat sp.]	2e-05
1474	AB013357	Mus musculus mRNA for 49 kDa zinc finger protein, complete cds	e-136	4153886	(AB013357) 49 kDa zinc finger protein	5e-08
1475	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	e-117	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	4e-32
1476	U38253	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds	e-103	2494312	TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) subunit [Rattus norvegicus]	3e-42

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1477	X73683	R.norvegicus mRNA for histone H3.3	e-117	122075	(H3.3Q) histone H3.3 - fruit fly (Drosophila melanogaster) histone H3.3B - chicken >gi 2119023 pir S61218 histone H3.3 - fruit fly (Drosophila hydei) 1-136) [Oryctolagus cuniculus] >gi 8046 (X53822) Histone H3.3Q gene product [Drosophila melanogaster] >gi 51198 gallus] >gi 161190 (M17876) histone H3 [Spisula solidissima] >gi 211853 (M11393) histone 3.3 [Gallus gallus] >gi 306848 (M11354) H3.3 histone [Homo sapiens] melanogaster] >gi 963031 (X81205) histone H3.3 H3.3A variant [Drosophila melanogaster] musculus]	1e-45
1478	U32498	Rattus norvegicus rsec8 mRNA, partial cds	e-108	2143962	rsec8 - rat (fragment) >gi 1019441 (U32498) rsec8 [Rattus norvegicus]	7e-48
1479	U41736	Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds	e-146	1517822	(U41736) ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]	5e-49
1480	AF041338	Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds	e-119	2895578	(AF041338) vacuolar proton pump subunit SFD alpha isoform [Bos taurus]	3e-49
1481	AF064553	Mus musculus NSD1 protein mRNA, complete cds	e-121	3329465	(AF064553) NSD1 protein [Mus musculus]	2e-50
1482	AB000517	Rattus sp. mRNA for CDP-diacylglycerol synthase, complete cds	e-146	1517822	(U41736) ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]	2e-51
1483	D38517	Mouse mRNA for Dhml protein, complete cds	e-118	2137562	mouse Dhml protein - mouse musculus]	6e-54

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1484	X54352	M.domesticus MD6 mRNA	e-139	1085499	CDC4 repeat unit-containing protein - mouse	1e-55
1485	U57692	Mus musculus N-terminal asparagine amidohydrolase (Ntan1) mRNA, complete cds	e-118	2498797	PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNA) >gi 1373365 (U57691) N-terminal asparagine amidohydrolase [Mus musculus] amidohydrolase [Mus musculus]	5e-57
1486	X80169	M.musculus mRNA for 200 kD protein	e-119	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi 1083553 pir A55117 tsg24	9e-58
1487	U57692	Mus musculus N-terminal asparagine amidohydrolase (Ntan1) mRNA, complete cds	e-120	2498797	PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNA) >gi 1373365 (U57691) N-terminal asparagine amidohydrolase [Mus musculus] amidohydrolase [Mus musculus]	8e-58
1488	U08215	Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.	e-109	473407	(U08215) NST-1 [Mus musculus]	7e-58
1489	D85926	Mouse mRNA for Ray, complete cds	e-110	1944389	(D85926) Ray [Mus musculus]	2e-58
1490	L20427	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds	e-123	457372	(L20427) dihydroxypolyprenylbenzoate methyltransferase dihydroxypolyprenylbenzoate methyltransferase [Rattus norvegicus]	4e-59
1491	X56044	M.musculus mRNA for protein Htf9C	e-121	3183977	(X56044) protein Htf9C [Mus musculus]	1e-60

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					PROTO-ONCOGENE	
1492	S74774	p59 ^{fyn} (T)=OKT3-induced calcium influx regulator	e-163	729896	TYROSINE-PROTEIN KINASE FYN (P59-FYN) >gi 420217 pir A44991 protein-tyrosine kinase (EC 2.7.1.112) fyn - mouse	8e-63
1493	U88873	Mus musculus BUB2-like protein 1 (HBLP1) mRNA, complete cds	e-123	4099611	(U88873) BUB2-like protein 1 [Mus musculus]	1e-63
1494	U48852	Cricetulus griseus HT protein mRNA, complete cds.	e-117	1216486	(U48852) HT protein [Cricetulus griseus]	7e-64
1495	AF032667	Rattus norvegicus rexo70 mRNA, complete cds	e-142	2827160	(AF032667) rexo70 [Rattus norvegicus]	5e-66
1496	M62722	Chinese hamster phosphatidylserine decarboxylase mRNA, 3' end.	e-114	118910	PHOSPHATIDYLSERINE DECARBOXYLASE PROENZYME >gi 109423 pir A38732 phosphatidylserine decarboxylase (EC 4.1.1.65) - Chinese hamster (fragment)	2e-67
1497	AF072758	Mus musculus fatty acid transport protein 3 mRNA, partial cds	e-130	3335567	(AF072758) fatty acid transport protein 3; FATP3 [Mus musculus]	1e-67
1498	AB005549	Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds	e-113	3868778	(AB005549) atypical PKC specific binding protein [Rattus norvegicus]	2e-69
1499	U57344	Mus musculus homeobox protein Meis3 mRNA, complete cds	e-143	3024124	HOMEBOX PROTEIN MEIS3	6e-72
1500	U09874	Mus musculus SKD3 mRNA, complete cds.	e-142	2493735	SKD3 PROTEIN SKD3 [Mus musculus]	1e-72
1501	U72194	Mus musculus muskelin mRNA, complete cds	e-148	3493462	(U72194) muskelin [Mus musculus]	2e-74
1502	XS0169	M.musculus mRNA for 200 kD protein	e-155	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi 1083553 pir A55117 tsg24	3e-77

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus muskelin mRNA, complete cds	e-154	3493462	(U72194) muskelin [Mus musculus]	2e-78
1503	U72194					
		Cricetulus griseus mRNA for Zn finger factor	e-146	3150148	(Y12836) Zn finger factor [Cricetulus griseus]	3e-83
1504	Y12836					

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Table 5

SEQ ID	Start	Stop	Score	Direction	Description
29	295	421	5872	For	mkk like kinases
30	31	182	3943	For	Basic region plus leucine zipper transcription factors
31	298	397	5625	For	mkk like kinases
186	175	395	7660	For	SH2 Domain
187	358	432	4320	For	Ank repeat
196	37	322	6049	For	mkk like kinases
234	23	121	4607	For	SH3 Domain
308	110	172	4150	For	Zinc finger, C2H2 type
410	42	191	4036	For	Basic region plus leucine zipper transcription factors
431	71	428	5538	Rev	ATPases Associated with Various Cellular Activities
552	116	288	3930	Rev	Basic region plus leucine zipper transcription factors
639	157	561	5797	For	ATPases Associated with Various Cellular Activities
746	209	427	5379	For	Fibronectin type III domain
768	116	288	3930	For	Basic region plus leucine zipper transcription factors
807	339	392	3620	For	Zinc finger, C2H2 type
820	341	406	2930	Rev	EF-hand
822	108	262	4179	For	Basic region plus leucine zipper transcription factors
836	158	353	4430	For	Basic region plus leucine zipper transcription factors
1157	41	444	5279	Rev	protein kinase
1192	186	416	5469	For	Fibronectin type III domain
1268	238	315	3540	For	Ank repeat
1269	79	240	11640	For	LIM domain containing proteins
1288	73	234	3953	For	Basic region plus leucine zipper transcription factors

SEQ ID	Start	Stop	Score	Direction	Description
1309	248	404	8226	for	LIM domain containing proteins
1324	294	356	4690	for	Zinc finger, C2H2 type
1325	1	234	8981	for	C2 domain (prot. kinase C like)
1336	66	164	6390	for	WD domain, G-beta repeats
1360	222	377	8686	for	LIM domain containing proteins
1365	69	257	5221	for	Basic region plus leucine zipper transcription factors
1380	42	140	7130	for	WD domain, G-beta repeats
1386	243	398	8736	for	LIM domain containing proteins
1410	222	350	10553	for	Trypsin
1417	8	354	6073	for	Protein Tyrosine Phosphatase
1454	49	209	3996	for	Basic region plus leucine zipper transcription factors
1464	4	180	4978	for	RNA recognition motif. (aka RRM, RBD, or RNP domain)
1478	54	437	5176	for	protein kinase
1496	241	520	3929	for	Helicases conserved C-terminal domain
1496	40	612	5187	for	protein kinase
1503	154	216	4870	for	Zinc finger, C2H2 type
1514	2	252	4662	for	RNA recognition motif. (aka RRM, RBD, or RNP domain)
1527	156	212	3520	for	Zinc finger, C2H2 type
1538	9	635	11087	for	wnt family of developmental signaling proteins
1540	289	471	4107	for	Basic region plus leucine zipper transcription factors
1549	200	391	4118	for	Basic region plus leucine zipper transcription factors
1556	163	354	3958	for	Basic region plus leucine zipper transcription factors
1557	207	398	4038	for	Basic region plus leucine zipper transcription factors
1563	107	298	3978	for	Basic region plus leucine zipper transcription factors

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SEQ ID	Start	Stop	Score	Direction	Description
1622	180	365	4022	for	Basic region plus leucine zipper transcription factors
1630	100	291	3998	for	Basic region plus leucine zipper transcription factors
1674	196	258	4880	for	Zinc finger, C2H2 type
1676	9	86	6610	for	Homeobox Domain
1677	316	369	5780	rev	Thioredoxins
1688	109	410	17414	for	Ras family
1704	184	372	3977	for	Basic region plus leucine zipper transcription factors
1707	92	439	24100	rev	Phosphatidylinositol-specific phospholipase C, Y domain
1711	263	361	6400	for	WD domain, G-beta repeats
1744	238	433	10572	rev	Serine carboxypeptidases
1755	281	367	2580	for	EF-hand
1762	236	334	5880	for	WD domain, G-beta repeats
1779	64	126	4790	for	Zinc finger, C2H2 type
1801	295	351	4030	for	Zinc finger, C2H2 type
1804	301	378	3460	for	Ank repeat
1808	36	161	4170	for	Basic region plus leucine zipper transcription factors
1811	184	315	8390	for	N-terminal homology in Ets domain
1814	127	294	10770	for	Bromodomain (conserved sequence found in human, Drosophila and yeast proteins.)
1818	9	146	4741	for	Double-stranded RNA binding motif
1819	278	355	3460	for	Ank repeat
1820	123	299	12150	for	Homeobox Domain
1821	127	303	12180	for	Homeobox Domain
1830	184	267	4270	for	Ank repeat
1832	18	173	8987	for	SH3 Domain
1835	51	206	8987	for	SH3 Domain
1839	224	307	4270	for	Ank repeat
1846	12	398	36700	for	G-protein alpha subunit

SEQ ID	Start	Stop	Score	Direction	Description
1909	160	258	6370	for	WD domain, G-beta repeats
1911	35	151	9335	for	Zinc finger, C3HC4 type (RING finger)
1980	60	197	7917	for	Zinc finger, C3HC4 type (RING finger)
2065	253	306	5410	for	Zinc finger, CCHC class
2135	2	401	10596	for	ATPases Associated with Various Cellular Activities
2216	90	179	5380	for	WW/rsp5/WWP domain containing proteins
2218	127	225	5500	for	WD domain, G-beta repeats
2281	20	387	6044	for	Protein Tyrosine Phosphatase
2282	183	353	5136	for	C2 domain (prot. kinase C like)
2286	12	382	5228	for	protein kinase
2310	20	371	5962	for	Protein Tyrosine Phosphatase
2363	48	211	4132	for	Basic region plus leucine zipper transcription factors
2424	43	194	3996	for	Basic region plus leucine zipper transcription factors
2428	25	350	4675	for	Dual specificity phosphatase, catalytic domain
2562	18	101	4560	for	Ank repeat
2577	0	311	10295	for	4 transmembrane segments integral membrane proteins
2591	60	165	4560	for	SH2 Domain
2684	9	461	5759	for	ATPases Associated with Various Cellular Activities
2826	116	400	16107	for	DEAD and DEAH box helicases
2859	100	320	5550	rev	ATPases Associated with Various Cellular Activities
2871	198	392	9384	for	DEAD and DEAH box helicases
2944	18	281	10480	for	Calpain large subunit, domain III
2969	5	387	5976	rev	protein kinase
3015	131	214	3600	for	Ank repeat
3047	191	292	5295	for	WD domain, G-beta repeats
3081	190	252	4360	for	Zinc finger, C2H2 type
3108	275	367	5791	for	WD domain, G-beta repeats
3147	190	369	4022	for	Basic region plus leucine zipper transcription factors
3152	129	320	3947	for	Basic region plus leucine zipper transcription factors
3158	167	334	4180	for	Basic region plus leucine zipper transcription factors
3175	14	164	5951	for	mkk like kinases

SEQ ID	Start	Stop	Score	Direction	Description
3175	8	112	5968	for	protein kinase
3178	45	386	19398	for	ATPases Associated with Various Cellular Activities
3183	14	215	9133	for	4 transmembrane segments integral membrane proteins
3190	229	390	6089	for	mkk like kinases
3190	118	390	8063	for	protein kinase
3193	293	355	3570	for	Zinc finger, C2H2 type
3195	0	215	10146	for	4 transmembrane segments integral membrane proteins
3197	281	343	4490	for	Zinc finger, C2H2 type
3208	34	256	4190	for	Basic region plus leucine zipper transcription factors
3258	138	394	9877	for	Ras family
3266	8	139	9328	for	ATPases Associated with Various Cellular Activities
3267	97	180	3820	for	Ank repeat
3274	11	187	15442	for	Fork head domain, eukaryotic transcription factors
3281	15	182	9681	for	mkk like kinases
3285	16	102	4680	for	EF-hand
3292	208	300	5585	for	WD domain, G-beta repeats
3297	7	153	6100	for	Helicases conserved C-terminal domain
3306	161	223	4900	for	Zinc finger, C2H2 type
3307	43	321	8740	for	SH2 Domain
3339	94	342	14970	for	SH2 Domain
3345	65	271	12512	for	PDZ domain
3351	124	270	6068	for	Phorbol esters/diacylglycerol binding

Example 4

DIFFERENTIAL EXPRESSION OF POLYNUCLEOTIDES OF THE INVENTION:
DESCRIPTION OF LIBRARIES AND DETECTION OF DIFFERENTIAL EXPRESSION

- 5 The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 6 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepare the cDNA library, the abbreviated name of the library that is used in the tables below (in quotes),
10 and the approximate number of clones in the library.

Table 6
Description of cDNA Libraries

Library (lib #)	Description	Number of Clones in this Clustering
1	Km12 L4 Human Colon Cell Line, High Metastatic Potential (derived from Km12C) "High Colon"	307133
2	Km12C Human Colon Cell Line, Low Metastatic Potential "Low Colon"	284755
3	MDA-MB-231 Human Breast Cancer Cell Line, High Metastatic Potential; micro-metastases in lung "High Breast"	326937
4	MCF7 Human Breast Cancer Cell, Non Metastatic "Low Breast"	318979
8	MV-522 Human Lung Cancer Cell Line, High Metastatic Potential "High Lung"	223620
9	UCP-3 Human Lung Cancer Cell Line, Low Metastatic Potential "Low Lung"	312503

Library (lib #)	Description	Number of Clones in this Clustering
12	Human microvascular endothelial cells (HMEC) – Untreated PCR (OligodT) cDNA library	41938
13	Human microvascular endothelial cells (HMEC) – Basic fibroblast growth factor (bFGF) treated PCR (OligodT) cDNA library	42100
14	Human microvascular endothelial cells (HMEC) – Vascular endothelial growth factor (VEGF) treated PCR (OligodT) cDNA library	42825
15	Normal Colon – UC#2 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	34285
16	Colon Tumor – UC#2 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	35625
17	Liver Metastasis from Colon Tumor of UC#2 Patient PCR (OligodT) cDNA library “High Colon Metastasis Tissue”	36984
18	Normal Colon – UC#3 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	36216
19	Colon Tumor – UC#3 Patient PCR (OligodT) cDNA library “High Colon Tumor Tissue”	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient PCR (OligodT) cDNA library “High Colon Metastasis Tissue”	30956
21	G RRPz Human Prostate Cell Line	164801
22	WOca Human Prostate Cancer Cell Line	162088

The KM12L4 and KM12C cell lines are described in Example 1 above.
The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer. Inst.* (1974) 53:661), is of high metastatic potential, and forms poorly
5 differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma.

The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, e.g., Chandrasekaran et al., *Cancer Res.* (1979) 39:870 (MDA-MB-231 and MCF-7); Gastpar et al., *J Med Chem* (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson et al., *Br J Cancer* (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang et al., *Nucleic Acids Res* (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki et al., *Int J Cancer* (1987) 40:46 (UCP-3); Varki et al., *Tumour Biol.* (1990) 11:327; (MV-522 and UCP-3); Varki et al., *Anticancer Res.* (1990) 10:637; (MV-522); Kelner et al., *Anticancer Res* (1995) 15:867 (MV-522); and Zhang et al., *Anticancer Drugs* (1997) 8:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz cell line refers to low passage (3 passages or fewer) human prostate cells, and the WOca cell line refers to low passage (3 passages or fewer) human prostate cancer cells.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac et al., *Genomics* (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may

occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones
5 can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones
10 corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in
15 the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the
20 second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially
25 expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5, where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974)).

EXAMPLE 5

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL
BREAST CANCER CELLS VERSUS LOW METASTATIC BREAST CANCER CELLS

5 A number of polynucleotide sequences have been identified that are
differentially expressed between cells derived from high metastatic potential breast
cancer tissue and low metastatic breast cancer cells. Expression of these sequences in
breast cancer can be valuable in determining diagnostic, prognostic and/or treatment
information. For example, sequences that are highly expressed in the high metastatic
10 potential cells can be indicative of increased expression of genes or regulatory
sequences involved in the metastatic process. A patient sample displaying an increased
level of one or more of these polynucleotides may thus warrant more aggressive
treatment. In another example, sequences that display higher expression in the low
metastatic potential cells can be associated with genes or regulatory sequences that
15 inhibit metastasis, and thus the expression of these polynucleotides in a sample may
warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a
diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the
like. These polynucleotide sequences can also be used in combination with other
20 known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially
expressed between high metastatic potential breast cancer cells and low metastatic
potential breast cancer cells.

Table 7

25 Differentially expressed polynucleotides: Higher expression in
high metastatic potential breast cancer (lib3) relative to low metastatic
breast cancer cells (lib4)

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
472	64	0	62
1851	6	0	6
1856	8	0	8
1867	6	0	6
1872	6	0	6
1875	12	3	4
1923	89	22	4

482

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
2118	7	0	7
2119	7	0	7
2135	37	13	3
2190	19	0	19
2193	16	5	3
2232	12	2	6
2239	6	0	6
2338	21	2	10
2378	16	4	4
2394	6	0	6
2395	6	0	6
2490	13	3	4
2505	16	2	8
2540	8	1	8
2542	11	1	11
2607	11	2	5
2640	22	5	4
2674	8	0	8
2679	19	0	19
2684	14	4	3
2707	8	0	8
2724	9	0	9
2757	6	0	6
2776	10	0	10
2804	13	2	6
2818	6	0	6
2906	14	0	14
2959	26	8	3
2964	17	4	4
2968	6	0	6
2977	22	3	7
2980	13	1	13
3010	6	0	6
3043	10	1	10
3071	33	12	3
3072	9	1	9
3095	19	3	6
3097	11	2	5
3173	12	2	6
3203	8	1	8
3210	27	8	3

A83

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
3212	13	1	13
3284	8	0	8
3288	6	0	6
3331	14	3	5
3335	13	1	13

Table 8

Differentially expressed polynucleotides: Higher expression in low metastatic breast cancer cells (lib4) relative to high metastatic potential breast cancer (lib3)

5

SEQ ID NOs:	Lib 3 Clones	Lib 4 Clones	lib4/lib3
402	0	6	6
614	3	21	7
624	0	6	6
626	0	8	8
712	0	9	9
744	0	7	7
1325	2	29	15
1452	2	13	7
1880	0	9	9
1915	0	7	7
1951	0	6	6
1955	8	32	4
2015	0	7	7
2046	0	7	7
2076	1	22	23
2087	0	6	6
2124	0	9	9
2145	0	8	8
2162	0	6	6
2163	0	12	12
2164	5	19	4
2172	2	15	8
2192	5	16	3
2244	20	43	2
2266	3	18	6
2313	24	56	2
2346	1	13	13

494

SEQ ID NOs:	Lib 3 Clones	Lib 4 Clones	lib4/lib3
2355	0	10	10
2371	0	6	6
2393	1	17	17
2404	1	21	22
2443	0	6	6
2460	0	11	11
2523	0	6	6
2575	1	10	10
2578	0	6	6
2584	1	17	17
2590	0	6	6
2609	1	9	9
2632	5	24	5
2714	5	24	5
2728	0	6	6
2752	1	14	14
2794	4	15	4
2826	0	7	7
2987	5	15	3
3005	1	14	14
3009	20	58	3
3047	4	17	4
3057	2	17	9
3075	2	11	6
3076	0	6	6
3102	0	6	6
3128	15	52	4
3132	15	52	4
3142	0	6	6
3187	22	49	2
3253	23	96	4
3282	19	46	2
3285	20	40	2
3346	0	9	9

EXAMPLE 6

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL LUNG
CANCER CELLS VERSUS LOW METASTATIC LUNG CANCER CELLS

5 A number of polynucleotide sequences have been identified that are
differentially expressed between cells derived from high metastatic potential lung
cancer cells and low metastatic lung cancer cells. Expression of these sequences in lung
cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment
information. For example, sequences that are highly expressed in the high metastatic
10 potential cells can be indicative of increased expression of genes or regulatory
sequences involved in the metastatic process. A patient sample displaying an increased
level of one or more of these polynucleotides may thus warrant more aggressive
treatment. In another example, sequences that display higher expression in the low
metastatic potential cells can be associated with genes or regulatory sequences that
15 inhibit metastasis, and thus the expression of these polynucleotides in a sample may
warrant a more positive prognosis than the gross pathology would suggest.

 The differential expression of these polynucleotides can be used as a
diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the
like. These polynucleotide sequences can also be used in combination with other
20 known molecular and/or biochemical markers.

 The following tables summarize polynucleotides that are differentially
expressed between high metastatic potential lung cancer cells and low metastatic
potential lung cancer cells:

Table 9

Differentially expressed polynucleotides: Higher expression in high
metastatic potential lung cancer cells (lib8) relative to low
metastatic lung cancer cells (lib9)

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
14	10	0	10
137	5	0	5
151	5	0	7
152	9	0	13
171	6	0	8
200	10	0	14
254	5	0	7
262	5	0	7
271	5	0	7
348	6	1	8
412	5	0	7
507	5	0	7
520	6	0	8
530	5	0	7
588	5	0	7
623	7	0	10
637	7	0	10
660	5	0	7
678	8	0	11
680	5	0	7
700	9	2	6
714	28	13	3
774	11	0	15
812	5	0	7
834	8	2	6
901	11	2	8
1168	5	0	7
1333	6	0	8
1352	5	0	7
1524	11	1	15
1706	5	0	7
1752	17	9	3
1768	20	4	7
1769	5	0	7
1780	6	0	8

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
1781	40	3	19
1799	6	1	8
1803	6	1	8
1811	16	9	2
1884	6	0	8
1919	8	1	11
1939	6	0	8
1975	43	9	7
2024	12	1	17
2045	8	1	11
2060	20	13	2
2071	16	4	6
2128	5	0	7
2177	10	2	7
2181	44	13	5
2184	11	1	15
2185	10	4	3
2283	7	0	10
2311	10	4	3
2314	10	0	14
2393	14	6	3
2398	6	1	8
2460	10	4	3
2514	6	0	8
2597	5	0	7
2657	8	2	6
2669	6	1	8
2670	6	1	8
3047	21	3	10
3050	16	5	4
3092	7	1	10
3140	181	119	2
3157	5	0	7
3187	16	5	4
3210	5	0	7
3220	28	4	10
3236	7	1	10
3249	16	0	22
3264	8	2	6
3305	7	0	10
3309	20	0	28

488

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
3318	24	4	8
3330	5	0	7
3331	5	0	7

Table 10

Differentially expressed polynucleotides: Higher expression in low metastatic lung cancer cells (lib 9) relative to high metastatic potential lung cancer cells (lib 8)

SEQ ID NO:	Lib 8 clones	Lib 9 clones	lib 9/lib 8
24	3	20	5
53	0	18	13
64	0	8	6
70	0	11	8
105	10	66	5
129	0	16	11
214	1	14	10
233	4	35	6
237	0	13	9
264	0	29	21
329	2	17	6
368	1	37	26
370	0	11	8
418	0	8	6
450	0	9	6
461	0	9	6
484	0	26	19
494	0	41	29
517	1	12	9
522	1	11	8
581	1	17	12
614	3	23	5
706	0	11	8
726	5	23	3
806	0	14	10
824	0	9	6
836	1	14	10
874	0	12	9
900	5	21	3
1017	2	14	5

489

SEQ ID NO:	Lib 8 clones	Lib 9 clones	lib 9/lib 8
1144	0	8	6
1154	0	12	9
1166	2	45	16
1170	1	13	9
1302	2	13	5
1326	1	13	9
1327	1	13	9
1367	0	12	9
1377	0	12	9
1437	2	18	6
1442	1	14	10
1466	0	13	9
1476	0	13	9
1495	0	8	6
1496	1	13	9
1664	38	253	5
1682	1	17	12
1687	0	9	6
1758	0	8	6
1817	4	18	3
1837	3	16	4
1845	3	23	5
1856	2	17	6
1910	1	18	13
2146	2	16	9
2156	0	9	6
2463	0	12	9
2724	10	38	3
2749	403	2000	4
2801	6	25	3
2993	3	18	4
3080	0	10	7
3107	3	23	5
3292	0	20	14
3324	110	548	4

EXAMPLE 7

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL
COLON CANCER CELLS VERSUS LOW METASTATIC COLON CANCER CELLS

5 A number of polynucleotide sequences have been identified that are
differentially expressed between cells derived from high metastatic potential colon
cancer cells and low metastatic colon cancer cells. Expression of these sequences in
colon cancer tissue can provide diagnostic, prognostic and/or treatment information.
For example, sequences that are highly expressed in the high metastatic potential cells
10 can be indicative of increased expression of genes or regulatory sequences involved in
the metastatic process. A patient sample displaying an increased level of one or more of
these polynucleotides may thus warrant more aggressive treatment. In another example,
sequences that display higher expression in the low metastatic potential cells can be
associated with genes or regulatory sequences that inhibit metastasis, and thus the
15 expression of these polynucleotides in a sample may warrant a more positive prognosis
than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a
diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the
like. These polynucleotide sequences can also be used in combination with other
20 known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with
differential expression between high metastatic potential colon cancer cells and low
metastatic potential colon cancer cells:

Table 11

25 Differentially expressed polynucleotides: Higher expression in low metastatic colon
cancer cells (lib 2) relative to high metastatic potential colon cancer cells (lib 1)

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
429	0	9	10
1494	0	8	9
1923	34	114	4
1986	3	12	4
2018	0	9	10
2036	2	10	5
2049	8	25	3
2135	24	87	4

491

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
2146	2	16	9
2208	6	27	5
2215	2	11	6
2239	1	10	11
2307	2	12	6
2313	28	62	2
2357	5	14	3
2360	3	21	8
2362	0	6	6
2378	3	12	4
2569	3	20	7
2571	0	6	6
2588	54	172	3
2592	15	41	3
2611	0	6	6
2636	0	9	10
2641	7	20	3
2650	0	9	10
2662	0	9	10
2674	4	13	4
2682	0	6	6
2702	9	25	3
2704	8	23	3
2715	2	12	6
2804	9	22	3
2821	13	29	2
2840	1	8	9
2846	2	15	8
2866	0	6	6
2906	0	6	6
2915	44	109	3
2933	0	6	6
2935	5	16	3
2957	1	11	12
2959	3	27	10
2977	16	30	2
2980	12	27	2
3000	2	13	7
3009	12	29	3
3115	0	7	8
3156	502	2170	5

482

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
3210	2	21	11
3211	0	9	10
3213	0	7	8
3235	2	12	6
3251	2	12	6
3296	3	12	4
3335	1	8	9

EXAMPLE 8

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL COLON CANCER PATIENT TISSUE VERSUS NORMAL PATIENT TISSUE

5

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the advanced disease state which involves processes such as angiogenesis, dedifferentiation, cell replication, and metastasis. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment.

15

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer tissue and normal colon tissue:

Table 12

Differentially expressed polynucleotides isolated from samples from two patients (patient 2 and patient 3 and) : Lower expression in high metastatic potential colon tissue (patient 2:lib 17; patient 3:lib 20) vs. normal colon tissue (patient 2:lib 15; patient 3:lib 18)

5

SEQ ID NO:	lib 15 clones	lib 17 clones	lib 15/lib 17
69	19	7	3
123	6	0	6
140	24	8	3
197	6	0	6
198	113	0	121
254	28	9	3
412	28	9	3
512	11	1	12
641	17	7	3
642	7	0	8
954	12	3	4
1011	209	16	14
1024	8	0	9
1040	12	3	4
1055	26	7	4
1106	31	15	2
1125	17	0	18
1129	17	0	18
1138	109	0	117
1244	14	1	15
1253	73	0	78
1283	34	7	5
1285	34	7	5
1339	13	4	3
1474	73	0	78
1505	18	3	6
1553	68	6	12
1554	2542	14	195
1605	2542	14	195
1628	6	0	6
1643	142	4	38
1753	12	0	10
1764	13	0	14

494

SEQ ID NO:	lib 15 clones	lib 17 clones	lib 15/lib 17
SEQ ID NO:	Lib18 Clones	Lib20 Clones	lib18/lib20
105	28	11	2
198	21	0	18
254	9	0	8
412	9	0	8
1011	11	1	9
1138	14	0	12
1253	23	0	20
1643	18	0	15
1764	12	0	10
3156	140	43	3

Table 13

Differentially expressed polynucleotides isolated from samples from two patients (patient 2 and patient 3): Lower expression in normal colon tissue (patient 2:lib 15; patient 3:lib 18)vs. high metastatic potential colon tissue (patient 2:lib 17; patient 3:lib 20).

SEQ ID NO:	Lib 15 Clones	Lib 17 Clones	lib 17/lib 15
321	3	23	7
363	1	9	8
836	21	99	4
859	6	20	3
885	13	28	2
916	13	28	2
981	2	11	5
1226	8	70	8
1308	0	8	7
1317	29	84	3
1429	27	127	4
1442	0	9	8
1534	1	12	11
1540	12	43	3
1552	0	7	7
1556	1	9	8
1557	1	9	8
1569	2189	5122	2
1571	6	18	3
1576	3	25	8

495

SEQ ID NO:	Lib 15 Clones	Lib 17 Clones	lib 17/lib 15
1581	4	22	5
1601	25	157	6
1613	9	48	5
1616	15	61	4
1620	2	17	8
1622	4	99	23
1626	6	35	5
1647	4	22	5
1664	4	28	7
1683	2	18	8
1704	3	15	5
1800	0	7	7
2749	23	60	2
2784	4	14	3
2805	1	9	8
2976	3	14	4
3128	18	57	3
3129	26	124	4
3146	64	210	3
3150	940	2267	2
3151	2	15	7
SEQ ID NO:	lib 18 clones	lib 20 clones	lib 20/lib 18
865	0	5	6
1569	1	7	8
1580	1	7	8
1590	1	7	8
2790	0	5	6

EXAMPLE 9

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH COLON TUMOR POTENTIAL
PATIENT TISSUE VERSUS METASTASIZED COLON CANCER PATIENT TISSUE

- 5 A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from colon cancer tissue and cells derived from colon cancer tissue metastases to liver. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information associated with the transformation of precancerous tissue to malignant tissue. This information

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can be useful in the prevention of achieving the advanced malignant state in these tissues, and can be important in risk assessment for a patient.

The following table summarizes identified polynucleotides with differential expression between high tumor potential colon cancer tissue and cells derived from high metastatic potential colon cancer cells:

Table 14

Differentially expressed polynucleotides:

Greater expression in metastatic colon tumor tissue (lib 20) vs.
colon tumor tissue (lib 19)

SEQ ID NO:	lib 19 clones	lib 20 clones	lib 20/lib 19
937	0	6	8
976	0	5	7
1520	1	8	11
1546	1	11	15
1550	1	11	15
1574	1	8	11
1580	0	7	9
1590	0	7	9
1599	8	21	4
1607	158	632	5
1622	1	7	9

Table 15

Greater expression in colon tumor tissue (lib 19) than metastatic colon tissue (lib 20)

SEQ ID NO:	lib 19 clones	lib 20 clones	lib 19/lib 20
105	64	11	4
1011	53	1	40
1226	18	4	3
1571	8	0	6
1726	15	3	4
1811	17	2	6
2749	47	6	6
3146	19	2	7
3324	20	1	15

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EXAMPLE 10

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH TUMOR POTENTIAL
COLON CANCER PATIENT TISSUE VERSUS NORMAL PATIENT TISSUE

5 A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information associated with the prevention of the malignant state in these tissues, and can be important in risk
10 assessment for a patient. For example, sequences that are highly expressed in the potential colon cancer cells are associated with or can be indicative of increased expression of genes or regulatory sequences involved in early tumor progression. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the
15 malignant state as early as possible.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer cells and normal colon cells:

Table 16

Differentially expressed polynucleotides detected in samples from patient (patient 2)
20 Higher expression in normal colon tissue (patient 2, lib 15)
vs. tumor potential colon tissue (patient 2:lib16)

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
69	19	7	3
105	116	54	2
140	24	4	6
197	6	0	6
198	113	3	40
254	28	6	5
412	28	6	5
642	7	0	7
830	10	2	5
938	31	13	3
1011	209	37	6
1095	12	3	4
1125	17	0	18

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
1129	17	0	18
1138	109	1	115
1253	73	1	77
1283	34	13	3
1285	34	13	3
1339	13	3	5
1453	11	3	4
1474	73	1	77
1505	18	6	3
1554	2542	448	6
1605	2542	448	6
1614	36	14	3
1630	24	9	3
1643	142	2	75
1646	39	14	3
1649	24	8	3
1677	19	6	3
1753	13	0	14
1764	13	0	14
1766	177	65	3
1772	24	8	3

Table 17

Differentially expressed polypeptides detected in samples from patient. Lower expression in normal colon tissue (lib 18) than colon tumor tissue (lib 19)

SEQ ID NO:	lib 18 clones	lib 19 clones	lib 19/lib 18
3146	3	19	6
3150	21	228	10
3324	3	20	6

Table 18

Differentially expressed polypeptides detected in samples from patient. Higher expression in normal colon tissue (lib 18) than colon tumor tissue (lib 19)

SEQ ID NO:	lib 18 clones	lib 19 clones	lib 18/lib 19
198	21	2	12
465	6	0	7
489	6	0	7
745	6	0	7
859	11	2	6
976	7	0	8
1011	209	37	6
1045	8	1	9
1138	14	0	16
1253	23	0	26
1392	16	4	5
1474	23	0	26
1589	6	0	7
1591	22	11	2
1607	386	158	3
1643	18	0	21
1753	12	0	14
1764	12	0	14
SEQ ID NO:	lib 18 clones	lib 19 clones	lib 19/lib 18
105	28	64	2
1011	11	53	4
1226	2	18	8
1251	6	19	3
1559	1	9	8
1571	0	8	7
1608	1	9	8
1766	2	13	6
1782	1	9	8
1811	1	17	15

Table 19

Differentially expressed polynucleotides:

Higher expression in colon tumor tissue

(patient 2, lib 16) vs. normal colon tissue (patient 2, lib 15)

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
7	1	9	9
164	6	19	3
734	4	15	4
836	21	53	2
928	2	11	5
965	2	11	5
987	2	11	5
1026	7	19	3
1044	4	16	4
1119	4	16	4
1226	8	46	5
1227	0	9	9
1251	7	95	13
1316	0	6	6
1429	27	81	3
1442	0	9	9
1540	12	28	2
1553	68	590	8
1560	4	24	6
1577	1	10	9
1588	5	20	4
1610	3	13	4
1620	2	23	11
1626	6	23	4
1673	2	15	7
2416	0	7	7
2749	23	54	2
2976	3	14	4
3129	26	64	2
3132	18	54	3

EXAMPLE 11

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN GROWTH FACTOR-STIMULATED
HUMAN MICROVASCULAR ENDOTHELIAL CELLS (HMEC) RELATIVE TO UNTREATED
HMEC

5 A number of polynucleotide sequences have been identified that are
differentially expressed between human microvascular endothelial cells (HMEC) that
have been treated with growth factors relative to untreated HMEC.

Sequences that are differentially expressed between growth factor-treated
HMEC and untreated HMEC can represent sequences encoding gene products involved
10 in angiogenesis, metastasis (cell migration), and other developmental and oncogenic
processes. For example, sequences that are more highly expressed in HMEC treated
with growth factors (such as bFGF or VEGF) relative to untreated HMEC can serve as
markers of cancer cells of higher metastatic potential. Detection of expression of these
sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment
15 information associated with the prevention of achieving the malignant state in these
tissues, and can be important in risk assessment for a patient. A patient sample
displaying an increased level of one or more of these polynucleotides may thus warrant
closer attention or more frequent screening procedures to catch the malignant state as
early as possible.

20 The following table summarizes identified polynucleotides with
differential expression between growth factor-treated and untreated HMEC.

Table 20

Differentially expressed polynucleotides:

25 Higher expression in untreated HMEC (lib 12) vs. bFGF treated HMEC (lib 13)

SEQ ID NO:	lib 12 clones	lib 13 clones	lib 12/lib 13
849	6	0	6
1059	6	0	6
1206	12	2	6
3208	12	0	12

Lower expression in untreated HMEC (lib 12) vs. bFGF treated HMEC (lib 13)

2748	3	12	4
3325	0	6	6

Table 21

Differentially expressed polynucleotides:

Higher expression in untreated HMEC (lib 12) VEGF treated HMEC (lib 14)

SEQ ID NO:	lib 12 clones	lib 14 clones	lib 12/lib 14
1150	9	0	9

5

Lower expression in untreated HMEC (lib 12) vs. VEGF treated HMEC (lib 14)

3324	22	50	2
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EXAMPLE 12

10 POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN NORMAL PROSTATE CELLS RELATIVE TO PROSTATE CANCER CELLS

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from normal prostate cells and prostate cancer cells. Expression of these sequences prostate tissue suspected of being cancerous can provide diagnostic, prognostic and/or treatment information. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers. The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and low metastatic potential colon cancer cells:

20

Table 22

Differentially expressed polynucleotides: normal prostate cell line (lib 21)
vs. prostate cancer cell line (lib 22)

Higher in lib 21

SEQ ID NO:	lib 21 clones	lib 22 clones	lib 21/lib 22
53	17	2	8
1754	22	8	3
1801	7	0	7
1845	22	6	4
446	8	0	8
1410	6	0	6
2060	18	6	3
2143	12	3	4
2632	13	1	13
2899	16	2	8
3338	12	2	6

5

Higher in lib 22

86	2	13	7
93	0	9	9
687	0	9	9
1269	1	15	15
1581	25	74	3
1647	25	74	3
1649	12	27	2
1710	5	16	3
1717	5	16	3
1772	12	27	2
1960	0	6	6
2987	0	6	6
3128	13	42	3
3132	13	42	3
3150	263	962	4
3222	0	6	6
3268	0	6	6

EXAMPLE 13

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED ACROSS MULTIPLE LIBRARIES

A number of polynucleotide sequences have been identified that are differentially expressed between cancerous cells and normal cells across two or more tissue types tested (*i.e.*, breast, colon, lung, and prostate). Expression of these sequences in a tissue of any origin can provide diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. These polynucleotides can also serve as non-tissue specific markers of, for example, risk of metastasis of a tumor. The following polynucleotides were differentially expressed but without tissue type-specificity in at least two of the breast, colon, lung, and prostate libraries tested: 53, 105, 355, 412, 614, 836, 1442, 1581, 1647, 1649, 1664, 1772, 1782, 1811, 1845, 1856, 1875, 1923, 2060, 2071, 2135, 2146, 2239, 2313, 2378, 2393, 2416, 2460, 2490, 2632, 2674, 2704, 2724, 2749, 2784, 2804, 2959, 2976, 2977, 2980, 2987, 3009, 3047, 3128, 3129, 3132, 3146, 3150, 3156, 3210, 3324, 3331, and 3335.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Deposit Information:

The following materials were deposited with the American Type Culture Collection (ATCC); CMCC = Chiron Master Culture Collection:

cDNA Libraries Deposited with ATCC

Tube Number	Deposit Date	ATCC Accession No.	CMCC Accession No.
ES137	May 30, 2000		
ES138	May 30, 2000		
ES139	May 30, 2000		
ES140	May 30, 2000		
ES141	May 30, 2000		
ES142	May 30, 2000		
ES143	May 30, 2000		
ES144	May 30, 2000		
ES145	May 30, 2000		
ES146	May 30, 2000		
ES147	May 30, 2000		
ES148	May 30, 2000		
ES149	May 30, 2000		
ES150	May 30, 2000		
ES151	May 30, 2000		
ES152	May 30, 2000		
ES153	May 30, 2000		
ES154	May 30, 2000		
ES155	May 30, 2000		
ES156	May 30, 2000		
ES157	May 30, 2000		
ES158	May 30, 2000		
ES159	May 30, 2000		
ES160	May 30, 2000		
ES161	May 30, 2000		
ES162	May 30, 2000		
ES163	May 30, 2000		
ES164	May 30, 2000		
ES165	May 30, 2000		
ES166	May 30, 2000		
ES167	May 30, 2000		

Table 23 lists the clones for each deposit, designated as "tube" number.

- 5 This deposit is provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences

herein. A license may be required to make, use, or sell the deposited material, and no such license is granted hereby.

Retrieval of Individual Clones from Deposit of Pooled Clones

Where the ATCC deposit is composed of a pool of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (e.g., a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, e.g., by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

Table 23

Clone Name	Tube
M00001351A:B02	ES 137
M00001356A:H11	ES 137
M00001363D:D09	ES 137
M00001395D:H02	ES 137
M00001439C:H06	ES 137
M00001476B:G10	ES 137
M00001582A:E02	ES 137
M00003750D:E06	ES 137
M00003761C:F02	ES 137
M00003770A:E05	ES 137
M00003786A:A11	ES 137
M00003800A:F09	ES 137
M00003816D:E11	ES 137
M00003902A:C03	ES 137
M00003991C:F06	ES 137

Clone Name	Tube
M00003995B:E03	ES 137
M00004046C:A08	ES 137
M00004105D:D05	ES 137
M00004139B:B10	ES 137
M00004140D:C03	ES 137
M00004144A:H05	ES 137
M00004152A:C12	ES 137
M00004155D:A10	ES 137
M00004168A:G11	ES 137
M00004197B:H10	ES 137
M00004222C:E03	ES 137
M00004234A:E07	ES 137
M00004239B:F11	ES 137
M00004241B:H07	ES 137
M00004264B:A05	ES 137

Clone Name	Tube
M00004278A:F09	ES 137
M00004282D:C11	ES 137
M00004308C:C06	ES 137
M00004340C:C07	ES 137
M00004354D:E05	ES 137
M00004361A:H02	ES 137
M00004372B:F07	ES 137
M00004378A:B10	ES 137
M00004393B:E07	ES 137
M00023282A:C02	ES 137
M00023300D:C11	ES 137
M00023316C:G08	ES 137
M00023333D:C12	ES 137
M00023352B:F03	ES 137
M00023352D:H03	ES 137
M00023376B:G04	ES 137
M00023377B:F01	ES 137
M00023398B:D12	ES 137
M00023399C:E10	ES 137
M00026803A:F08	ES 137
M00026843B:D10	ES 137
M00026850D:F09	ES 137
M00026851B:F01	ES 137
M00026856D:F02	ES 137
M00026857D:G12	ES 137
M00026859D:D01	ES 137
M00026860B:C05	ES 137
M00026865B:A06	ES 137
M00026868C:E11	ES 137
M00026878A:F05	ES 137
M00026882D:G09	ES 137
M00026885A:H09	ES 137
M00026901A:G07	ES 137
M00026914A:H10	ES 137
M00026915B:C06	ES 137
M00026918B:D01	ES 137
M00026922C:B02	ES 137
M00026922C:G03	ES 137
M00026926A:E10	ES 137
M00026927D:F02	ES 137
M00026928D:A03	ES 137
M00026935C:B04	ES 137
M00026941D:A04	ES 137
M00026944B:E03	ES 137
M00026946A:F12	ES 137

Clone Name	Tube
M00026980A:D09	ES 137
M00027016A:B06	ES 137
M00027018A:C09	ES 137
M00027021A:G02	ES 137
M00027022D:G11	ES 137
M00027030C:H06	ES 137
M00027035D:C06	ES 137
M00027049B:F05	ES 137
M00027078A:B02	ES 137
M00027080A:B01	ES 137
M00027085C:E11	ES 137
M00027094A:B03	ES 137
M00027103B:A09	ES 137
M00027108C:B03	ES 137
M00027121D:C05	ES 137
M00027135A:B11	ES 137
M00027136C:C09	ES 137
M00027141C:H03	ES 137
M00027159D:F03	ES 137
M00027162B:F05	ES 137
M00027178B:G09	ES 137
M00027179D:E06	ES 138
M00027181D:A05	ES 138
M00027195C:E04	ES 138
M00027198B:B08	ES 138
M00027200A:F02	ES 138
M00027207B:F07	ES 138
M00027212D:E03	ES 138
M00027228D:A01	ES 138
M00027232D:B08	ES 138
M00027233B:C01	ES 138
M00027236A:E04	ES 138
M00027237C:B08	ES 138
M00027248A:C02	ES 138
M00027256B:H09	ES 138
M00027258A:A07	ES 138
M00027263A:F10	ES 138
M00027292D:F10	ES 138
M00027297A:C04	ES 138
M00027299B:B12	ES 138
M00027301A:G05	ES 138
M00027301B:B08	ES 138
M00027314C:D09	ES 138
M00027319D:B11	ES 138
M00027324D:C05	ES 138

Clone Name	Tube
M00027347C:G07	ES 138
M00027355A:B07	ES 138
M00027359B:G05	ES 138
M00027366A:F11	ES 138
M00027379C:B07	ES 138
M00027392B:H02	ES 138
M00027396D:G08	ES 138
M00027398C:F07	ES 138
M00027438C:G07	ES 138
M00027462A:D07	ES 138
M00027462B:H07	ES 138
M00027468A:C09	ES 138
M00027475B:E10	ES 138
M00027476A:C09	ES 138
M00027486A:F06	ES 138
M00027520A:C05	ES 138
M00027525B:D06	ES 138
M00027526D:F03	ES 138
M00027528C:B10	ES 138
M00027537C:B01	ES 138
M00027546C:B10	ES 138
M00027591B:C04	ES 138
M00027596A:A10	ES 138
M00027596C:E06	ES 138
M00027602B:C01	ES 138
M00027615A:F10	ES 138
M00027617B:C12	ES 138
M00027620D:F11	ES 138
M00027625A:H01	ES 138
M00027634A:D11	ES 138
M00027641C:A03	ES 138
M00027647C:D03	ES 138
M00027652B:F11	ES 138
M00027668C:H12	ES 138
M00027729D:H06	ES 138
M00027733A:A02	ES 138
M00027741B:F09	ES 138
M00027743A:C03	ES 138
M00027801C:C11	ES 138
M00027813C:F01	ES 138
M00027818C:C07	ES 138
M00027836D:F12	ES 138
M00027837C:D09	ES 138
M00028120D:F12	ES 138
M00028066C:D07	ES 138

Clone Name	Tube
M00028184D:G10	ES 138
M00028185B:A06	ES 138
M00028196D:A03	ES 138
M00028201B:H12	ES 138
M00028207D:E09	ES 138
M00028210B:D02	ES 138
M00028212C:B08	ES 138
M00028215D:F03	ES 138
M00028220A:B04	ES 138
M00028314D:F05	ES 138
M00028316B:H12	ES 138
M00028354A:B12	ES 138
M00028354D:A03	ES 138
M00028357A:G10	ES 138
M00028362A:G11	ES 138
M00028364C:G08	ES 138
M00028369D:E08	ES 138
M00028617C:A12	ES 138
M00028768C:D05	ES 138
M00028770A:D04	ES 138
M00028772C:B09	ES 138
M00028775D:F03	ES 138
M00028777B:G12	ES 138
M00031368A:E10	ES 138
M00031417C:G09	ES 138
M00031419D:C04	ES 138
M00031485D:G02	ES 138
M00032480B:E10	ES 139
M00032492A:C01	ES 139
M00032495B:D02	ES 139
M00032499C:A01	ES 139
M00032508B:H03	ES 139
M00032510D:F12	ES 139
M00032510D:G06	ES 139
M00032513D:F01	ES 139
M00032530D:C02	ES 139
M00032535D:H01	ES 139
M00032539B:C11	ES 139
M00032540A:A09	ES 139
M00032541D:H08	ES 139
M00032545B:H09	ES 139
M00032545D:G05	ES 139
M00032550D:C02	ES 139
M00032551B:G05	ES 139
M00032577A:C04	ES 139

Clone Name	Tube
M00032578A:G06	ES 139
M00032584A:H08	ES 139
M00032592A:H11	ES 139
M00032597C:B01	ES 139
M00032638C:G08	ES 139
M00032638D:A06	ES 139
M00032668D:G12	ES 139
M00032678C:D06	ES 139
M00032688D:D11	ES 139
M00032712B:G02	ES 139
M00032724A:C05	ES 139
M00032725C:F06	ES 139
M00032726C:C01	ES 139
M00032731B:C10	ES 139
M00032731C:C07	ES 139
M00032737B:E09	ES 139
M00032739A:A06	ES 139
M00032744B:F10	ES 139
M00032766B:D12	ES 139
M00032766C:A04	ES 139
M00032790B:A07	ES 139
M00032793A:F06	ES 139
M00032797B:G02	ES 139
M00032808B:G10	ES 139
M00032811B:D02	ES 139
M00032829B:E06	ES 139
M00032830D:G03	ES 139
M00032831C:G07	ES 139
M00032853D:G12	ES 139
M00032864B:B09	ES 139
M00032871D:E11	ES 139
M00032876C:D06	ES 139
M00032907A:G04	ES 139
M00032909A:B06	ES 139
M00032917D:G09	ES 139
M00032918B:D08	ES 139
M00032918B:E06	ES 139
M00032918C:B10	ES 139
M00032921B:H08	ES 139
M00032933A:C10	ES 139
M00032939B:E07	ES 139
M00032940A:C02	ES 139
M00032942D:C12	ES 139
M00032944B:B02	ES 139
M00032984C:G05	ES 139

Clone Name	Tube
M00032990B:A11	ES 139
M00032994A:A08	ES 139
M00032995C:C05	ES 139
M00033007C:E01	ES 139
M00033019B:E10	ES 139
M00033033C:H01	ES 139
M00033034C:A06	ES 139
M00033034C:F02	ES 139
M00033037D:C11	ES 139
M00033074A:C08	ES 139
M00033130B:F06	ES 139
M00033140D:F06	ES 139
M00033173D:C01	ES 139
M00033176B:E12	ES 139
M00033186C:D11	ES 139
M00033189D:F08	ES 139
M00033202D:G06	ES 139
M00033204B:A07	ES 139
M00033205A:F03	ES 139
M00033217B:H07	ES 139
M00033218A:C04	ES 139
M00033223B:H07	ES 139
M00033226A:A11	ES 139
M00033231D:B09	ES 139
M00033231D:G10	ES 139
M00033243B:A05	ES 139
M00033246C:E08	ES 139
M00033248A:B02	ES 139
M00033261C:D12	ES 139
M00033262D:A11	ES 139
M00033263B:G04	ES 139
M00033276B:G08	ES 139
M00033185C:D01	ES 139
M00033288B:D12	ES 140
M00033300D:H12	ES 140
M00033306D:G08	ES 140
M00033306D:H09	ES 140
M00033308B:G05	ES 140
M00033343C:H08	ES 140
M00033345D:A09	ES 140
M00033346C:A05	ES 140
M00033347C:F02	ES 140
M00033349D:F05	ES 140
M00033358A:H12	ES 140
M00033362C:C05	ES 140

Clone Name	Tube
M00033375A:G04	ES 140
M00033376A:C12	ES 140
M00033377D:A05	ES 140
M00033410B:C09	ES 140
M00033424B:A04	ES 140
M00033424D:H12	ES 140
M00033425A:C10	ES 140
M00033427D:F01	ES 140
M00033432B:H10	ES 140
M00033437C:A07	ES 140
M00033437C:C03	ES 140
M00033442A:D06	ES 140
M00033446C:G08	ES 140
M00033446D:B02	ES 140
M00033450C:A02	ES 140
M00033451A:H01	ES 140
M00033454A:D09	ES 140
M00033457D:A05	ES 140
M00033560D:G07	ES 140
M00033561C:A02	ES 140
M00033566C:E08	ES 140
M00033570B:C08	ES 140
M00033570B:E06	ES 140
M00033570C:C10	ES 140
M00033578D:G02	ES 140
M00033581C:H10	ES 140
M00033581D:D08	ES 140
M00033583B:E06	ES 140
M00033583D:B05	ES 140
M00033584D:G11	ES 140
M00033585D:A02	ES 140
M00033588C:G04	ES 140
M00033594C:B03	ES 140
M00033595A:C11	ES 140
M00038259A:G08	ES 140
M00038259B:A02	ES 140
M00038259B:G08	ES 140
M00038259C:H09	ES 140
M00038272A:G01	ES 140
M00038272D:F11	ES 140
M00038279C:A11	ES 140
M00038284B:H04	ES 140
M00038303A:C03	ES 140
M00038303C:D02	ES 140
M00038303D:E07	ES 140

Clone Name	Tube
M00038315C:G11	ES 140
M00038325D:F12	ES 140
M00038326B:D04	ES 140
M00038327A:C11	ES 140
M00038327D:A05	ES 140
M00038328D:A03	ES 140
M00038329A:E08	ES 140
M00038387B:A07	ES 140
M00038614C:H11	ES 140
M00038615A:H12	ES 140
M00038616D:B12	ES 140
M00038618C:C08	ES 140
M00038619B:A03	ES 140
M00038620B:E09	ES 140
M00038631C:B10	ES 140
M00038631D:B02	ES 140
M00038632C:B09	ES 140
M00038633A:D07	ES 140
M00038633B:G02	ES 140
M00038635A:G09	ES 140
M00038635B:C08	ES 140
M00038638D:H03	ES 140
M00038639B:C03	ES 140
M00038639D:F07	ES 140
M00038661A:A07	ES 140
M00038662B:A12	ES 140
M00038663B:H06	ES 140
M00038663D:H10	ES 140
M00038664C:E04	ES 140
M00038991A:D01	ES 140
M00038994A:A10	ES 140
M00038995C:G08	ES 140
M00038995D:E05	ES 140
M00038999B:G11	ES 140
M00038999D:C11	ES 140
M00039002D:G11	ES 140
M00039004B:A06	ES 140
M00039004B:C11	ES 140
M00039005C:H01	ES 141
M00039006D:B01	ES 141
M00039011D:C10	ES 141
M00039013A:C09	ES 141
M00039013D:F02	ES 141
M00039014A:H10	ES 141
M00039014B:C04	ES 141

Clone Name	Tube
M00039015A:D07	ES 141
M00039015B:G10	ES 141
M00039015B:H09	ES 141
M00039015D:H04	ES 141
M00039016A:A02	ES 141
M00039016D:G06	ES 141
M00039024B:B10	ES 141
M00039025A:H09	ES 141
M00039026D:F05	ES 141
M00039028C:B11	ES 141
M00039030B:E02	ES 141
M00039036C:B05	ES 141
M00039039B:E03	ES 141
M00039039B:F09	ES 141
M00039042B:B02	ES 141
M00039043B:E01	ES 141
M00039049D:G07	ES 141
M00039050A:H10	ES 141
M00039052C:F07	ES 141
M00039058A:A04	ES 141
M00039058C:H02	ES 141
M00039059C:G08	ES 141
M00039061B:F08	ES 141
M00039063B:D08	ES 141
M00039064D:H09	ES 141
M00039066D:G08	ES 141
M00039068B:B04	ES 141
M00039068C:E06	ES 141
M00039070D:C02	ES 141
M00039072C:C03	ES 141
M00039072C:E02	ES 141
M00039079A:A05	ES 141
M00039080C:H06	ES 141
M00039081B:G06	ES 141
M00039082B:A05	ES 141
M00039084C:G07	ES 141
M00039084C:H03	ES 141
M00039084C:H04	ES 141
M00039084D:D07	ES 141
M00039096A:A05	ES 141
M00039096A:E07	ES 141
M00039097D:D06	ES 141
M00039099A:H08	ES 141
M00039104D:C09	ES 141
M00039105C:B08	ES 141

Clone Name	Tube
M00039107C:E04	ES 141
M00039108D:B06	ES 141
M00039112B:C05	ES 141
M00039118B:C05	ES 141
M00039118D:A06	ES 141
M00039120C:C09	ES 141
M00039120C:H03	ES 141
M00039123A:B10	ES 141
M00039124C:F03	ES 141
M00039124C:H02	ES 141
M00039124C:H08	ES 141
M00039126D:A08	ES 141
M00039127A:G11	ES 141
M00039127D:E10	ES 141
M00039129C:D04	ES 141
M00039133B:F08	ES 141
M00039135D:F05	ES 141
M00039135D:G02	ES 141
M00039135D:H02	ES 141
M00039139A:C09	ES 141
M00039139C:G12	ES 141
M00039140A:B08	ES 141
M00039140D:A04	ES 141
M00039140D:D09	ES 141
M00039141C:E01	ES 141
M00039142D:B11	ES 141
M00039144C:E06	ES 141
M00039147A:F10	ES 141
M00039156A:B11	ES 141
M00039158B:G12	ES 141
M00039166B:G06	ES 141
M00039167B:H09	ES 141
M00039168C:A04	ES 141
M00039169A:E12	ES 141
M00039170A:B10	ES 141
M00039170C:F05	ES 141
M00039171B:D11	ES 141
M00039177B:D03	ES 141
M00039179A:G09	ES 141
M00039180A:A07	ES 141
M00039196B:H06	ES 141
M00039196D:A07	ES 141
M00039200A:C10	ES 141
M00039211A:C12	ES 141
M00039212C:C12	ES 142

Clone Name	Tube
M00039213A:D01	ES 142
M00039213B:F05	ES 142
M00039218A:F03	ES 142
M00039221A:H03	ES 142
M00039224A:E12	ES 142
M00039228A:B05	ES 142
M00039230A:A10	ES 142
M00039230D:D09	ES 142
M00039230D:G12	ES 142
M00039233A:A03	ES 142
M00039238A:B12	ES 142
M00039238D:A08	ES 142
M00039241A:E11	ES 142
M00039249A:C12	ES 142
M00039249C:G11	ES 142
M00039255C:E12	ES 142
M00039257D:C03	ES 142
M00039258B:E06	ES 142
M00039258D:B08	ES 142
M00039260C:G03	ES 142
M00039263D:A12	ES 142
M00039266A:B02	ES 142
M00039266D:F12	ES 142
M00039266D:H04	ES 142
M00039273B:F02	ES 142
M00039273D:B02	ES 142
M00039274B:G07	ES 142
M00039276B:H09	ES 142
M00039277D:G10	ES 142
M00039279B:C11	ES 142
M00039279B:H02	ES 142
M00039279C:B08	ES 142
M00039281D:B04	ES 142
M00039284D:B12	ES 142
M00039286A:C06	ES 142
M00039287C:A06	ES 142
M00039288C:B11	ES 142
M00039293A:H04	ES 142
M00039293B:C11	ES 142
M00039295B:D03	ES 142
M00039297C:H08	ES 142
M00039298B:B06	ES 142
M00039298B:D03	ES 142
M00039298D:B04	ES 142
M00039299B:G12	ES 142

Clone Name	Tube
M00039300C:C09	ES 142
M00039300C:G04	ES 142
M00039301B:F06	ES 142
M00039303C:F11	ES 142
M00039304D:B09	ES 142
M00039308B:G08	ES 142
M00039310A:C07	ES 142
M00039313D:G04	ES 142
M00039316A:C01	ES 142
M00039318B:B09	ES 142
M00039319B:H12	ES 142
M00039319C:A04	ES 142
M00039322A:F04	ES 142
M00039328D:D07	ES 142
M00039329A:C01	ES 142
M00039329C:B10	ES 142
M00039333D:D09	ES 142
M00039334B:E03	ES 142
M00039335A:E08	ES 142
M00039339A:H07	ES 142
M00039339C:F03	ES 142
M00039340A:D05	ES 142
M00039340B:E07	ES 142
M00039340B:G08	ES 142
M00039341C:H11	ES 142
M00039341D:D07	ES 142
M00039343B:F12	ES 142
M00039344B:G07	ES 142
M00039345A:D09	ES 142
M00039345C:C12	ES 142
M00039381C:H08	ES 142
M00039381D:C02	ES 142
M00039384C:E02	ES 142
M00039384C:F08	ES 142
M00039385B:E09	ES 142
M00039391D:F08	ES 142
M00039396D:B04	ES 142
M00039397B:H09	ES 142
M00039398A:B10	ES 142
M00039401B:D02	ES 142
M00039402B:E03	ES 142
M00039403A:G12	ES 142
M00039404B:A05	ES 142
M00039407B:G02	ES 142
M00039411C:E07	ES 142

Clone Name	Tube
M00039412D:G06	ES 142
M00039414D:G03	ES 142
M00039415D:E01	ES 142
M00039417A:D03	ES 142
M00039417A:E12	ES 142
M00039417B:F01	ES 143
M00039417C:A01	ES 143
M00039417C:G01	ES 143
M00039418B:D08	ES 143
M00039420D:D03	ES 143
M00039422D:F04	ES 143
M00039425C:G01	ES 143
M00039425D:E12	ES 143
M00039428C:E01	ES 143
M00039430B:F12	ES 143
M00039431B:F04	ES 143
M00039432C:A01	ES 143
M00039444C:H02	ES 143
M00039452C:G09	ES 143
M00039454B:A11	ES 143
M00039455D:H04	ES 143
M00039456A:C08	ES 143
M00039458B:H11	ES 143
M00039461A:F04	ES 143
M00039465A:A08	ES 143
M00039472C:B08	ES 143
M00039475C:E10	ES 143
M00039476B:A02	ES 143
M00039477A:B03	ES 143
M00039477D:A10	ES 143
M00039611D:D11	ES 143
M00039612B:B10	ES 143
M00039612B:G05	ES 143
M00039616A:B10	ES 143
M00039616B:C01	ES 143
M00039619B:D02	ES 143
M00039631A:C10	ES 143
M00039633D:D05	ES 143
M00039636C:D11	ES 143
M00039637C:A10	ES 143
M00039652B:D05	ES 143
M00039655B:H09	ES 143
M00039655C:C07	ES 143
M00039655C:E08	ES 143
M00039660C:C10	ES 143

Clone Name	Tube
M00039663C:G09	ES 143
M00039664D:G07	ES 143
M00039672D:D10	ES 143
M00039673A:F09	ES 143
M00039675D:B03	ES 143
M00039675D:H05	ES 143
M00039677A:B08	ES 143
M00039681B:H09	ES 143
M00039682A:C08	ES 143
M00039682C:H11	ES 143
M00039684D:B08	ES 143
M00039685A:A08	ES 143
M00039686C:C05	ES 143
M00039686C:E06	ES 143
M00039688C:G06	ES 143
M00039689C:E08	ES 143
M00039696A:E05	ES 143
M00039697B:F11	ES 143
M00039700B:D02	ES 143
M00039702A:B12	ES 143
M00039702A:B02	ES 143
M00039705D:F02	ES 143
M00039707A:D02	ES 143
M00039710C:G03	ES 143
M00039720D:D02	ES 143
M00039727C:B09	ES 143
M00039729A:A10	ES 143
M00039771C:E11	ES 143
M00039773D:A09	ES 143
M00039773D:F11	ES 143
M00039774C:A03	ES 143
M00039774C:C09	ES 143
M00039775A:A09	ES 143
M00039777C:E05	ES 143
M00039778B:G03	ES 143
M00039778C:A04	ES 143
M00039781D:D10	ES 143
M00039782A:H10	ES 143
M00039785D:G05	ES 143
M00039788A:E03	ES 143
M00039788B:A06	ES 143
M00039788C:A01	ES 143
M00039790B:D03	ES 143
M00039792A:B04	ES 143
M00039793D:C05	ES 143

Clone Name	Tube
M00039794A:E04	ES 143
M00039795B:H10	ES 143
M00039795D:E10	ES 143
M00039795D:G06	ES 143
M00039797C:G05	ES 143
M00039798B:B02	ES 143
M00039799A:D10	ES 143
M00039801A:H11	ES 143
M00039807A:D01	ES 143
M00039808D:H02	ES 143
M00039810A:H10	ES 143
M00039813B:B01	ES 144
M00039813B:D11	ES 144
M00039815C:F09	ES 144
M00039816B:D04	ES 144
M00039816C:D05	ES 144
M00039820A:F11	ES 144
M00039820A:H11	ES 144
M00039820B:B06	ES 144
M00039827B:F07	ES 144
M00039828B:C05	ES 144
M00039832A:B12	ES 144
M00039835A:F07	ES 144
M00039838A:F05	ES 144
M00039839B:B01	ES 144
M00039839C:E05	ES 144
M00039847A:F06	ES 144
M00039851B:G11	ES 144
M00039851C:D12	ES 144
M00039854B:F09	ES 144
M00039855C:F01	ES 144
M00039857B:G10	ES 144
M00039859A:F06	ES 144
M00039859C:G10	ES 144
M00039864A:A07	ES 144
M00039866B:A08	ES 144
M00039869B:F06	ES 144
M00039875D:A10	ES 144
M00039876D:H09	ES 144
M00039877C:C03	ES 144
M00039879C:F05	ES 144
M00039879D:B11	ES 144
M00039880A:H11	ES 144
M00039884A:H11	ES 144
M00039885C:D01	ES 144

Clone Name	Tube
M00039887C:E07	ES 144
M00039887D:C04	ES 144
M00039888B:D03	ES 144
M00039890A:H05	ES 144
M00039894C:H07	ES 144
M00039896C:H01	ES 144
M00039897D:C10	ES 144
M00039898A:A08	ES 144
M00039898D:C06	ES 144
M00039903A:H07	ES 144
M00039903C:D01	ES 144
M00039903C:F03	ES 144
M00039909C:G05	ES 144
M00039909D:C02	ES 144
M00039910C:G10	ES 144
M00039914D:G12	ES 144
M00039915D:C11	ES 144
M00039927A:F04	ES 144
M00039928B:G05	ES 144
M00039936C:C05	ES 144
M00039938C:A08	ES 144
M00039938C:E11	ES 144
M00039940A:D07	ES 144
M00039940D:G08	ES 144
M00039973D:C08	ES 144
M00039973D:D12	ES 144
M00039975C:C11	ES 144
M00039976D:A12	ES 144
M00039978A:G03	ES 144
M00039981A:E08	ES 144
M00039982C:H04	ES 144
M00039983D:A06	ES 144
M00039984A:C02	ES 144
M00039984B:G12	ES 144
M00039984D:G12	ES 144
M00039987A:F09	ES 144
M00039987C:E12	ES 144
M00039987C:G08	ES 144
M00039988A:E06	ES 144
M00039990C:D10	ES 144
M00040004D:B03	ES 144
M00040005B:C11	ES 144
M00040005D:B07	ES 144
M00040007D:A06	ES 144
M00040009D:B07	ES 144

Clone Name	Tube
M00040010A:F10	ES 144
M00040014B:D01	ES 144
M00040014D:D10	ES 144
M00040014D:F03	ES 144
M00040015C:F08	ES 144
M00040016C:H12	ES 144
M00040017A:C06	ES 144
M00040017D:G03	ES 144
M00040019A:E01	ES 144
M00040021A:F09	ES 144
M00040022C:D06	ES 144
M00040026B:F06	ES 144
M00040029A:B03	ES 144
M00040029A:G04	ES 144
M00040031A:E06	ES 144
M00040032A:B03	ES 144
M00040032A:D09	ES 144
M00040037A:E11	ES 145
M00040038D:G04	ES 145
M00040039D:D06	ES 145
M00040040A:A06	ES 145
M00040041C:C09	ES 145
M00040042B:A10	ES 145
M00040047C:F05	ES 145
M00040052D:F12	ES 145
M00040055D:A06	ES 145
M00040055D:B01	ES 145
M00040060C:H10	ES 145
M00040062B:B05	ES 145
M00040070B:B07	ES 145
M00040071B:A10	ES 145
M00040072C:G09	ES 145
M00040076C:D06	ES 145
M00040077D:C11	ES 145
M00040080C:C06	ES 145
M00040081C:E01	ES 145
M00040085D:A10	ES 145
M00040085D:E04	ES 145
M00040087D:F08	ES 145
M00040088C:E10	ES 145
M00040089A:G08	ES 145
M00040089B:E04	ES 145
M00040089C:E06	ES 145
M00040090B:G09	ES 145
M00040092B:F05	ES 145

Clone Name	Tube
M00040093B:C02	ES 145
M00040093D:D03	ES 145
M00040097A:C12	ES 145
M00040098C:B01	ES 145
M00040098D:E04	ES 145
M00040098D:G12	ES 145
M00040100C:E05	ES 145
M00040100D:B06	ES 145
M00040103B:H10	ES 145
M00040105C:F11	ES 145
M00040106B:B09	ES 145
M00040107B:H07	ES 145
M00040111C:D05	ES 145
M00040115B:A04	ES 145
M00040115B:H12	ES 145
M00040118D:G10	ES 145
M00040121B:C05	ES 145
M00040122D:A02	ES 145
M00040123A:A09	ES 145
M00040124D:H01	ES 145
M00040129D:E10	ES 145
M00040302C:A04	ES 145
M00040304B:F06	ES 145
M00040305A:D11	ES 145
M00040305C:H06	ES 145
M00040307B:F01	ES 145
M00040307C:F10	ES 145
M00040309A:E11	ES 145
M00004825D:D05	ES 145
M00004832D:H02	ES 145
M00004839C:H02	ES 145
M00005018A:B05	ES 145
M00005297D:H08	ES 145
M00005308A:D06	ES 145
M00005351C:G05	ES 145
M00005352C:A02	ES 145
M00005358B:B06	ES 145
M00005359A:D04	ES 145
M00005379A:E04	ES 145
M00005382B:F08	ES 145
M00005384A:C11	ES 145
M00005402B:F08	ES 145
M00005445D:B01	ES 145
M00005449B:B10	ES 145
M00005449B:D01	ES 145

Clone Name	Tube
M00005457C:A03	ES 145
M00005458A:F11	ES 145
M00005498A:H06	ES 145
M00005531D:F06	ES 145
M00005539D:G01	ES 145
M00005555A:A10	ES 145
M00005556B:D02	ES 145
M00005601D:D08	ES 145
M00005614B:B01	ES 145
M00005623A:G02	ES 145
M00005623D:G12	ES 145
M00005625A:C02	ES 145
M00005673B:B12	ES 145
M00005778B:F09	ES 145
M00005805D:D12	ES 145
M00005820C:E04	ES 145
M00006581D:F08	ES 145
M00006599D:B02	ES 145
M00006657C:G05	ES 145
M00006680B:D02	ES 145
M00006712C:H09	ES 145
M00006809B:B09	ES 145
M00006861B:F09	ES 145
M00006866A:D07	ES 146
M00006886D:H02	ES 146
M00006893C:E07	ES 146
M00006897A:H02	ES 146
M00006928D:D07	ES 146
M00006935C:F06	ES 146
M00006968A:G08	ES 146
M00006977C:G04	ES 146
M00006977D:A03	ES 146
M00007012D:H08	ES 146
M00007013A:D09	ES 146
M00007026B:H09	ES 146
M00007108B:A02	ES 146
M00007112C:B10	ES 146
M00007116C:G02	ES 146
M00007124D:H10	ES 146
M00007136A:A03	ES 146
M00007149A:G02	ES 146
M00007157C:F11	ES 146
M00007165B:G11	ES 146
M00007194A:B09	ES 146
M00007929C:B08	ES 146

Clone Name	Tube
M00007941D:C09	ES 146
M00007943D:C09	ES 146
M00007972B:H12	ES 146
M00007976A:C10	ES 146
M00007992C:F06	ES 146
M00007994A:G02	ES 146
M00008006B:B03	ES 146
M00008026B:C11	ES 146
M00008045A:H02	ES 146
M00008053A:F10	ES 146
M00008063B:A06	ES 146
M00021665B:F12	ES 146
M00021671D:F12	ES 146
M00021852D:A05	ES 146
M00021866D:A03	ES 146
M00021908D:G12	ES 146
M00021919C:A10	ES 146
M00021923C:D11	ES 146
M00021955A:H02	ES 146
M00021964C:E10	ES 146
M00021972D:C11	ES 146
M00022005C:C06	ES 146
M00022015B:B07	ES 146
M00022054A:H03	ES 146
M00022084D:B01	ES 146
M00022099B:D06	ES 146
M00022105C:C12	ES 146
M00022127C:H03	ES 146
M00022135C:B05	ES 146
M00022138A:E05	ES 146
M00022175D:D12	ES 146
M00022178B:D06	ES 146
M00022181C:D01	ES 146
M00022183B:C02	ES 146
M00022184C:C11	ES 146
M00022233C:A12	ES 146
M00022234C:D06	ES 146
M00022247A:E02	ES 146
M00022257A:B09	ES 146
M00022262D:G03	ES 146
M00022264B:G10	ES 146
M00022363C:G12	ES 146
M00022365D:A03	ES 146
M00022373A:B05	ES 146
M00022373C:B07	ES 146

Clone Name	Tube
M00022391B:E01	ES 146
M00022391D:F10	ES 146
M00022416A:A07	ES 146
M00022421B:C11	ES 146
M00022433A:E02	ES 146
M00022434D:D06	ES 146
M00022440B:E01	ES 146
M00022444D:G01	ES 146
M00022467C:B12	ES 146
M00022489C:G04	ES 146
M00022492C:A02	ES 146
M00022495D:H08	ES 146
M00022496B:E12	ES 146
M00022499A:B02	ES 146
M00022533A:A08	ES 146
M00022579C:C11	ES 146
M00022597D:A06	ES 146
M00022602A:E09	ES 146
M00022615D:G05	ES 146
M00022634D:C08	ES 146
M00022640C:C12	ES 146
M00022641C:H05	ES 146
M00022646A:H10	ES 146
M00022662D:G11	ES 146
M00022667D:B02	ES 146
M00022668B:B12	ES 146
M00022670D:H11	ES 146
M00022671B:A08	ES 146
M00022684A:C02	ES 146
M00022731A:D02	ES 147
M00022739A:B03	ES 147
M00022747D:E03	ES 147
M00022767B:G11	ES 147
M00022785C:G06	ES 147
M00022793D:B01	ES 147
M00022795B:G06	ES 147
M00022797B:G08	ES 147
M00022817A:H02	ES 147
M00022821C:C09	ES 147
M00022823C:C01	ES 147
M00022830D:D01	ES 147
M00022834B:G11	ES 147
M00022854A:B03	ES 147
M00022856C:A07	ES 147
M00022860C:G04	ES 147

Clone Name	Tube
M00022885C:H05	ES 147
M00022895A:H08	ES 147
M00022910A:A06	ES 147
M00022925C:A08	ES 147
M00022928B:C01	ES 147
M00022930C:E02	ES 147
M00022938B:F07	ES 147
M00022968B:E02	ES 147
M00022976C:F04	ES 147
M00022979A:D05	ES 147
M00022986D:H09	ES 147
M00022997A:F06	ES 147
M00023001C:C08	ES 147
M00023003C:D07	ES 147
M00023007A:H04	ES 147
M00023007C:E10	ES 147
M00023020C:G08	ES 147
M00023024D:F12	ES 147
M00023032A:B05	ES 147
M00023039D:B05	ES 147
M00023042D:D02	ES 147
M00023044B:D02	ES 147
M00023094A:B11	ES 147
M00023100A:E12	ES 147
M00039181D:E05	ES 147
M00039184A:D03	ES 147
M00039184B:B09	ES 147
M00039361B:E01	ES 147
M00039363A:C09	ES 147
M00039366C:B07	ES 147
M00039367B:H02	ES 147
M00039371B:H06	ES 147
M00039372C:D12	ES 147
M00039374B:B07	ES 147
M00039374C:H12	ES 147
M00039374C:H02	ES 147
M00039376D:H07	ES 147
M00039377D:E12	ES 147
M00039378D:H07	ES 147
M00039379A:B03	ES 147
M00039380C:C09	ES 147
M00039482B:G02	ES 147
M00039493A:C04	ES 147
M00039496B:D08	ES 147
M00039496B:H09	ES 147

Clone Name	Tube
M00039497C:C06	ES 147
M00039499C:A04	ES 147
M00039500C:C04	ES 147
M00039505C:E03	ES 147
M00039508A:C12	ES 147
M00039508C:G01	ES 147
M00039510C:G02	ES 147
M00039512C:D06	ES 147
M00039515A:A06	ES 147
M00039515D:C11	ES 147
M00039517B:G12	ES 147
M00039521A:A02	ES 147
M00039521D:H03	ES 147
M00039528B:B12	ES 147
M00039529C:D07	ES 147
M00039530B:E02	ES 147
M00039533A:C12	ES 147
M00039533B:G08	ES 147
M00039533D:F04	ES 147
M00039535D:D10	ES 147
M00039536C:C10	ES 147
M00039536C:H11	ES 147
M00039561A:B07	ES 147
M00039561B:A09	ES 147
M00039562B:G02	ES 147
M00039564B:C01	ES 147
M00039570A:D10	ES 147
M00039570B:D10	ES 147
M00039584C:C01	ES 147
M00039584C:C11	ES 147
M00039587C:F12	ES 147
M00039590D:D02	ES 147
M00039591C:D06	ES 147
M00039595C:E05	ES 147
M00039597D:F04	ES 147
M00039600A:A11	ES 148
M00039604B:E05	ES 148
M00039604D:G03	ES 148
M00039606B:D08	ES 148
M00039607D:E08	ES 148
M00039608D:H01	ES 148
M00039609D:F07	ES 148
M00039624A:H09	ES 148
M00039624B:F12	ES 148
M00039625B:G08	ES 148

Clone Name	Tube
M00039626D:F04	ES 148
M00039629B:F01	ES 148
M00039629D:B04	ES 148
M00039630A:C08	ES 148
M00039630C:H04	ES 148
M00039641A:A05	ES 148
M00039641C:D07	ES 148
M00039642D:B12	ES 148
M00039642D:H09	ES 148
M00039643C:B04	ES 148
M00039645C:E01	ES 148
M00039647A:H11	ES 148
M00039736D:G08	ES 148
M00039740B:F10	ES 148
M00039752B:G08	ES 148
M00039755A:B08	ES 148
M00039756B:H06	ES 148
M00039760B:B08	ES 148
M00040131B:D11	ES 148
M00040131C:F03	ES 148
M00040131D:G08	ES 148
M00040133B:B03	ES 148
M00040136C:F08	ES 148
M00040138B:H03	ES 148
M00040141D:F05	ES 148
M00040143A:H05	ES 148
M00040145D:D03	ES 148
M00040147D:H11	ES 148
M00040160B:A10	ES 148
M00040162A:E01	ES 148
M00040169B:F08	ES 148
M00040173D:B05	ES 148
M00040174C:E10	ES 148
M00040174D:G03	ES 148
M00040181B:H09	ES 148
M00040181D:H10	ES 148
M00040182D:D06	ES 148
M00040183A:F07	ES 148
M00040184C:A11	ES 148
M00040191A:B09	ES 148
M00040221A:G11	ES 148
M00040222D:G02	ES 148
M00040223A:C05	ES 148
M00040226A:H10	ES 148
M00040230A:H02	ES 148

Clone Name	Tube
M00040231B:C08	ES 148
M00040232D:B07	ES 148
M00040233A:H02	ES 148
M00040233C:G05	ES 148
M00040252C:C06	ES 148
M00040253C:A05	ES 148
M00040254B:C10	ES 148
M00040256A:A06	ES 148
M00040257D:H10	ES 148
M00040260B:D02	ES 148
M00040260C:D04	ES 148
M00040261C:F01	ES 148
M00040262B:B06	ES 148
M00040264D:G05	ES 148
M00040265D:B07	ES 148
M00040265D:C08	ES 148
M00040267A:E06	ES 148
M00040267C:C04	ES 148
M00040271B:E12	ES 148
M00040271C:D08	ES 148
M00040273B:H12	ES 148
M00040274A:D07	ES 148
M00040274A:H11	ES 148
M00040280C:H05	ES 148
M00040281D:B01	ES 148
M00040282A:A03	ES 148
M00040286C:C02	ES 148
M00040287C:B09	ES 148
M00040287D:D07	ES 148
M00039746C:A08	ES 148
M00039746C:G09	ES 148
M00039746C:H05	ES 148
M00039746C:H06	ES 148
M00039746D:D11	ES 148
M00039748A:F11	ES 148
M00039748C:F11	ES 148
M00039749D:D05	ES 148
M00039761D:E10	ES 148
M00039762B:F07	ES 148
M00039764C:D07	ES 148
M00039766A:G07	ES 148
M00039766D:H01	ES 149
M00039767B:A04	ES 149
M00039767C:E12	ES 149
M00039770A:G11	ES 149

Clone Name	Tube
M00039770C:E04	ES 149
M00039942D:C01	ES 149
M00039943B:F10	ES 149
M00039945C:F09	ES 149
M00039946B:F08	ES 149
M00039947A:D06	ES 149
M00039947C:G03	ES 149
M00039948A:E03	ES 149
M00039948D:D11	ES 149
M00039951A:B07	ES 149
M00039951B:B12	ES 149
M00039951B:C03	ES 149
M00039955C:C04	ES 149
M00039957C:C09	ES 149
M00039957D:A12	ES 149
M00039958A:A08	ES 149
M00039958C:B09	ES 149
M00040201C:G11	ES 149
M00040202A:F05	ES 149
M00040203A:H06	ES 149
M00040203B:A05	ES 149
M00040203D:H11	ES 149
M00040206A:A07	ES 149
M00040207B:D08	ES 149
M00040208A:C03	ES 149
M00040208B:A07	ES 149
M00040208D:G09	ES 149
M00040217D:B07	ES 149
M00040218C:C02	ES 149
M00040219B:D02	ES 149
M00040219D:E08	ES 149
M00040291D:C05	ES 149
M00040293D:G04	ES 149
M00040294D:D12	ES 149
M00040296D:E09	ES 149
M00040298B:G02	ES 149
M00040299B:F10	ES 149
M00040313C:D05	ES 149
M00040313D:E04	ES 149
M00040314D:H05	ES 149
M00040317A:H03	ES 149
M00040317D:F02	ES 149
M00040318A:B02	ES 149
M00040318C:H11	ES 149
M00040320D:F02	ES 149

Clone Name	Tube
M00040323B:C12	ES 149
M00040323C:G11	ES 149
M00040326A:F04	ES 149
M00040327B:G06	ES 149
M00040332D:B05	ES 149
M00040333D:G05	ES 149
M00040334D:B02	ES 149
M00040334D:C07	ES 149
M00040342B:D12	ES 149
M00040345D:A09	ES 149
M00040346A:C11	ES 149
M00040347D:F09	ES 149
M00040349D:B09	ES 149
M00040351B:F02	ES 149
M00040351D:A11	ES 149
M00040364A:E05	ES 149
M00040366A:B01	ES 149
M00040368A:A12	ES 149
M00040368A:F01	ES 149
M00040368D:E09	ES 149
M00040371C:H05	ES 149
M00040375C:B06	ES 149
M00040376C:G02	ES 149
M00040377C:G07	ES 149
M00040383A:H02	ES 149
M00040383D:C04	ES 149
M00040385C:D02	ES 149
M00040386A:A02	ES 149
M00040387C:E07	ES 149
M00040387D:H05	ES 149
M00040390A:H02	ES 149
M00040390B:F02	ES 149
M00040391A:D10	ES 149
M00040392B:H01	ES 149
M00040392C:B12	ES 149
M00040394A:D04	ES 149
M00040395B:D11	ES 149
M00042534A:A05	ES 149
M00042538B:E06	ES 149
M00042543C:G04	ES 149
M00042558A:F03	ES 149
M00042560A:F12	ES 149
M00042565C:A08	ES 149
M00042566C:C05	ES 149
M00042567B:H10	ES 149

Clone Name	Tube
M00042693D:E04	ES 149
M00042696B:E05	ES 149
M00042697D:C07	ES 150
M00042698D:D10	ES 150
M00042698D:E01	ES 150
M00042702B:G02	ES 150
M00042704A:F09	ES 150
M00042711B:A11	ES 150
M00042717A:C07	ES 150
M00042737C:H04	ES 150
M00042740A:E09	ES 150
M00042742D:D05	ES 150
M00042887C:D07	ES 150
M00042895A:D10	ES 150
M00042895C:G01	ES 150
M00042902D:B08	ES 150
M00042904B:E07	ES 150
M00042905A:F11	ES 150
M00042905B:C03	ES 150
M00042905D:D02	ES 150
M00042347D:H11	ES 150
M00042348B:E05	ES 150
M00042349D:D07	ES 150
M00042431B:G08	ES 150
M00042431C:F01	ES 150
M00042431D:C10	ES 150
M00042432D:E02	ES 150
M00042435A:A11	ES 150
M00042436B:H09	ES 150
M00042437A:D04	ES 150
M00042439B:B03	ES 150
M00042439B:D03	ES 150
M00042440B:E09	ES 150
M00042463A:F09	ES 150
M00042470C:E05	ES 150
M00042511A:H04	ES 150
M00042515C:F08	ES 150
M00042751C:C12	ES 150
M00042752A:E11	ES 150
M00042756B:F11	ES 150
M00042756D:A10	ES 150
M00042759B:G11	ES 150
M00042760A:C12	ES 150
M00042765C:D04	ES 150
M00042767B:G10	ES 150

Clone Name	Tube
M00042769C:E09	ES 150
M00042770B:B12	ES 150
M00042770C:C04	ES 150
M00042771C:F06	ES 150
M00042774C:C05	ES 150
M00042781A:A07	ES 150
M00042784A:H06	ES 150
M00042788C:F11	ES 150
M00042790C:C07	ES 150
M00042792A:H01	ES 150
M00042797D:D10	ES 150
M00042799D:F08	ES 150
M00042800A:A03	ES 150
M00042802C:C04	ES 150
M00042806C:F07	ES 150
M00042807D:D05	ES 150
M00042823C:C02	ES 150
M00042830B:E02	ES 150
M00042839B:B11	ES 150
M00042841D:H07	ES 150
M00042849D:F11	ES 150
M00042852B:A03	ES 150
M00042852C:A01	ES 150
M00042856B:H02	ES 150
M00042352C:H03	ES 150
M00042352D:C01	ES 150
M00042352D:G09	ES 150
M00042448A:C09	ES 150
M00042448C:H12	ES 150
M00042453B:G09	ES 150
M00042518D:A06	ES 150
M00042518D:D04	ES 150
M00043296B:G09	ES 150
M00043304B:D05	ES 150
M00043304C:D02	ES 150
M00043305B:G02	ES 150
M00043306C:B03	ES 150
M00043306D:B07	ES 150
M00043310C:G06	ES 150
M00043311C:E03	ES 150
M00043312C:E08	ES 150
M00043320B:A07	ES 150
M00043324D:H11	ES 150
M00043328D:H02	ES 150
M00043332C:G04	ES 150

Clone Name	Tube
M00043334B:A10	ES 150
M00043338B:A03	ES 150
M00043338B:C11	ES 150
M00043339A:F11	ES 150
M00043340B:H08	ES 150
M00043344D:E04	ES 150
M00043345C:A06	ES 150
M00043346A:G01	ES 150
M00043350D:B11	ES 151
M00043351D:A11	ES 151
M00043352D:B05	ES 151
M00043352D:C03	ES 151
M00043359B:D10	ES 151
M00043359C:G01	ES 151
M00043361B:A01	ES 151
M00043366A:A02	ES 151
M00043366C:H05	ES 151
M00043367B:A08	ES 151
M00043368C:F09	ES 151
M00043370B:C08	ES 151
M00043372C:G05	ES 151
M00043377A:C03	ES 151
M00043378A:H10	ES 151
M00043379D:H02	ES 151
M00043383C:F12	ES 151
M00043383D:A02	ES 151
M00043384B:B02	ES 151
M00043386A:B08	ES 151
M00043389C:E03	ES 151
M00043389D:D07	ES 151
M00043391A:C10	ES 151
M00043391A:G08	ES 151
M00043392D:C11	ES 151
M00043393A:B08	ES 151
M00043401D:G08	ES 151
M00043402C:D08	ES 151
M00043405A:D11	ES 151
M00043405C:G12	ES 151
M00043405C:G02	ES 151
M00043406B:G12	ES 151
M00043407C:E05	ES 151
M00043408B:D11	ES 151
M00043409B:B03	ES 151
M00043410C:A09	ES 151
M00043411B:D08	ES 151

Clone Name	Tube
M00043411D:H06	ES 151
M00042584B:C10	ES 151
M00042623D:D07	ES 151
M00042625C:B04	ES 151
M00042626B:D08	ES 151
M00042627C:D01	ES 151
M00042630A:C05	ES 151
M00042955C:D05	ES 151
M00042956C:B06	ES 151
M00042960D:H08	ES 151
M00042962D:C05	ES 151
M00042964D:A03	ES 151
M00042966B:F07	ES 151
M00042966C:E06	ES 151
M00042970C:A04	ES 151
M00042970C:H10	ES 151
M00042976A:H04	ES 151
M00042979B:E02	ES 151
M00042981B:D11	ES 151
M00042983C:A11	ES 151
M00042983C:G06	ES 151
M00042986C:G12	ES 151
M00042988A:F06	ES 151
M00042997B:D06	ES 151
M00042998A:E03	ES 151
M00042998A:G04	ES 151
M00043001B:H10	ES 151
M00043001D:D03	ES 151
M00043002A:E05	ES 151
M00043003C:D08	ES 151
M00043011A:H12	ES 151
M00043015A:H10	ES 151
M00043022A:E12	ES 151
M00043026C:D07	ES 151
M00043028A:G05	ES 151
M00043029C:A06	ES 151
M00043032C:A10	ES 151
M00043034D:C01	ES 151
M00043036C:E05	ES 151
M00043036D:C09	ES 151
M00043040B:B07	ES 151
M00043044B:A12	ES 151
M00043044D:A09	ES 151
M00043045D:G12	ES 151
M00043046D:B11	ES 151

Clone Name	Tube
M00043060D:G12	ES 151
M00043066B:H11	ES 151
M00043067D:D10	ES 151
M00043125A:B11	ES 151
M00043125C:A11	ES 151
M00042611A:A06	ES 151
M00042611D:B12	ES 151
M00042612D:F06	ES 151
M00042614B:B05	ES 151
M00043073A:C12	ES 151
M00043078D:D04	ES 151
M00043081D:F05	ES 151
M00043087B:G07	ES 151
M00043093C:G11	ES 151
M00043095A:F09	ES 152
M00043096A:G04	ES 152
M00043108A:F06	ES 152
M00043109C:G01	ES 152
M00043131B:A09	ES 152
M00043133B:C11	ES 152
M00043138D:B11	ES 152
M00043143B:A10	ES 152
M00043148C:A09	ES 152
M00043154A:B07	ES 152
M00043162A:B08	ES 152
M00043162D:C12	ES 152
M00043164C:E12	ES 152
M00043165B:G01	ES 152
M00043173D:G03	ES 152
M00043184A:H08	ES 152
M00043187A:C04	ES 152
M00043191A:A07	ES 152
M00043192C:B12	ES 152
M00043200A:H09	ES 152
M00043200B:C08	ES 152
M00043202B:F01	ES 152
M00043203A:B09	ES 152
M00043210C:E05	ES 152
M00043211A:F01	ES 152
M00043213B:B12	ES 152
M00043215A:D02	ES 152
M00043220B:C04	ES 152
M00042591D:H03	ES 152
M00042592A:H10	ES 152
M00042593A:C02	ES 152

Clone Name	Tube
M00042593C:G06	ES 152
M00042595A:A11	ES 152
M00042595A:B01	ES 152
M00042596B:F06	ES 152
M00042596C:D07	ES 152
M00042597B:E12	ES 152
M00043416C:A02	ES 152
M00043417C:D05	ES 152
M00043418A:H10	ES 152
M00043419D:A10	ES 152
M00043428D:G08	ES 152
M00043430B:C02	ES 152
M00043431D:B08	ES 152
M00043433B:G09	ES 152
M00043433C:G07	ES 152
M00043437D:D04	ES 152
M00043440C:B07	ES 152
M00043446C:E12	ES 152
M00043447A:C07	ES 152
M00043449A:E12	ES 152
M00043450C:C06	ES 152
M00043453B:B09	ES 152
M00043458A:B12	ES 152
M00043461D:C02	ES 152
M00043461D:E06	ES 152
M00043465B:H02	ES 152
M00043465C:A03	ES 152
M00043465C:C09	ES 152
M00043476A:F07	ES 152
M00043483B:G10	ES 152
M00043491C:F04	ES 152
M00043492A:E01	ES 152
M00043513D:G08	ES 152
M00043516B:H09	ES 152
M00043518B:D06	ES 152
M00043526B:D10	ES 152
M00043527C:E09	ES 152
M00043528C:A02	ES 152
M00043616B:F02	ES 152
M00043616C:A05	ES 152
M00043632D:F09	ES 152
M00043634A:C10	ES 152
M00043635C:C11	ES 152
M00043636B:C06	ES 152
M00043637C:H01	ES 152

Clone Name	Tube
M00043638A:D06	ES 152
M00043640C:E03	ES 152
M00043648A:G07	ES 152
M00043649B:E07	ES 152
M00001338C:B02	ES 153
M00001338C:F05	ES 153
M00001338D:D01	ES 153
M00001340D:F07	ES 153
M00001344D:E08	ES 153
M00001346B:G11	ES 153
M00001348B:B03	ES 153
M00001349C:B04	ES 153
M00001351B:E11	ES 153
M00001352B:B02	ES 153
M00001353A:H07	ES 153
M00001353C:A05	ES 153
M00001353D:E05	ES 153
M00001356D:E06	ES 153
M00001358A:E08	ES 153
M00001359A:H10	ES 153
M00001361A:C12	ES 153
M00001361B:A12	ES 153
M00001362A:F09	ES 153
M00001364A:C09	ES 153
M00001364C:H10	ES 153
M00001368A:A08	ES 153
M00001368A:B07	ES 153
M00001368A:C02	ES 153
M00001369A:G06	ES 153
M00001374A:B02	ES 153
M00001374C:B10	ES 153
M00001375B:D04	ES 153
M00001378C:E10	ES 153
M00001379A:F09	ES 153
M00001382D:A07	ES 153
M00001382D:H08	ES 153
M00001384A:A07	ES 153
M00001385A:E07	ES 153
M00001386B:F11	ES 153
M00001387A:C12	ES 153
M00001387B:A11	ES 153
M00001389B:E10	ES 153
M00001389D:D06	ES 153
M00001390D:E02	ES 153
M00001391D:D03	ES 153

Clone Name	Tube
M00001393B:C03	ES 153
M00001393C:E08	ES 153
M00001393C:F04	ES 153
M00001393D:E02	ES 153
M00001396B:B01	ES 153
M00001396B:B12	ES 153
M00001396D:H02	ES 153
M00001397C:H08	ES 153
M00001399B:B01	ES 153
M00001399C:A01	ES 153
M00001403C:B03	ES 153
M00001403D:C12	ES 153
M00001406B:H09	ES 153
M00001406D:F06	ES 153
M00001410A:G10	ES 153
M00001416B:A05	ES 153
M00001421B:E07	ES 153
M00001422B:D06	ES 153
M00001424B:H06	ES 153
M00001424D:D02	ES 153
M00001426C:F06	ES 153
M00001428B:C10	ES 153
M00001429B:G05	ES 153
M00001430B:C01	ES 153
M00001433B:E02	ES 153
M00001442A:F08	ES 153
M00001442C:G12	ES 153
M00001444B:E04	ES 153
M00001444C:D11	ES 153
M00001445B:F06	ES 153
M00001449B:H10	ES 153
M00001451C:E10	ES 153
M00001460C:E10	ES 153
M00001461D:B10	ES 153
M00001461D:C10	ES 153
M00001465C:A02	ES 153
M00001466B:F03	ES 153
M00001467C:D04	ES 153
M00001477D:G09	ES 153
M00001485C:F06	ES 153
M00001488C:A03	ES 153
M00001497C:F10	ES 153
M00001503B:H10	ES 153
M00001506B:D11	ES 153
M00001512D:F08	ES 153

Clone Name	Tube
M00001518B:D10	ES 153
M00001528C:C03	ES 153
M00001532A:G08	ES 153
M00001533C:G11	ES 153
M00001533D:A01	ES 153
M00001534C:E07	ES 153
M00001535B:B10	ES 153
M00001535B:E02	ES 153
M00001537B:H10	ES 153
M00001538B:A07	ES 153
M00001539C:F12	ES 154
M00001542B:F09	ES 154
M00001543C:A08	ES 154
M00001544B:B05	ES 154
M00001544B:E06	ES 154
M00001546B:C11	ES 154
M00001548B:D06	ES 154
M00001550A:H06	ES 154
M00001550D:B11	ES 154
M00001551D:D01	ES 154
M00001551D:H09	ES 154
M00001554C:G10	ES 154
M00001558A:E06	ES 154
M00001559A:H09	ES 154
M00001561D:H04	ES 154
M00001562B:B02	ES 154
M00001562D:B07	ES 154
M00001565A:H05	ES 154
M00001568C:A03	ES 154
M00001570A:B07	ES 154
M00001591B:H05	ES 154
M00001596A:D02	ES 154
M00001600B:G01	ES 154
M00001605B:B05	ES 154
M00001606B:A10	ES 154
M00001606D:D06	ES 154
M00001607A:E04	ES 154
M00001607D:H09	ES 154
M00001609D:C11	ES 154
M00001616D:F03	ES 154
M00001617C:F10	ES 154
M00001618C:D01	ES 154
M00001619C:H09	ES 154
M00001620B:A03	ES 154
M00001623D:A10	ES 154

Clone Name	Tube
M00001623D:E12	ES 154
M00001624A:C01	ES 154
M00001625D:B04	ES 154
M00001626A:D07	ES 154
M00001632C:A10	ES 154
M00001633D:C11	ES 154
M00001637D:C12	ES 154
M00001648A:D10	ES 154
M00001661D:F06	ES 154
M00001663A:A12	ES 154
M00001671A:H10	ES 154
M00001671C:F03	ES 154
M00001675B:D06	ES 154
M00001677B:H08	ES 154
M00001680A:A01	ES 154
M00001683B:F11	ES 154
M00001684D:E04	ES 154
M00001686B:H01	ES 154
M00001686D:F06	ES 154
M00001688B:B11	ES 154
M00001692C:C04	ES 154
M00001771B:E06	ES 154
M00003746C:E11	ES 154
M00003749C:C08	ES 154
M00003753A:C11	ES 154
M00003758B:D07	ES 154
M00003758B:F06	ES 154
M00003760C:G10	ES 154
M00003761B:B02	ES 154
M00003763A:B02	ES 154
M00003763B:B10	ES 154
M00003764A:H09	ES 154
M00003764B:F11	ES 154
M00003764B:H11	ES 154
M00003764D:F07	ES 154
M00003768D:D08	ES 154
M00003770C:A10	ES 154
M00003771D:A03	ES 154
M00003773A:F10	ES 154
M00003780A:G01	ES 154
M00003782A:B02	ES 154
M00003785D:F07	ES 154
M00003787D:A10	ES 154
M00003808A:F11	ES 154
M00003808B:E07	ES 154

Clone Name	Tube
M00003812C:A03	ES 154
M00003814A:G05	ES 154
M00003819B:B01	ES 154
M00003820B:F11	ES 154
M00003821C:E12	ES 154
M00003822C:A09	ES 154
M00003822D:A02	ES 154
M00003823B:A06	ES 154
M00003825A:H10	ES 154
M00003828A:D11	ES 154
M00003830B:C06	ES 154
M00003830C:D02	ES 154
M00003837C:D10	ES 154
M00003839C:H10	ES 154
M00003842D:D11	ES 154
M00003842D:H09	ES 154
M00003845A:C07	ES 155
M00003845D:G03	ES 155
M00003847A:H04	ES 155
M00003848C:G09	ES 155
M00003851B:A01	ES 155
M00003854B:F07	ES 155
M00003855C:F02	ES 155
M00003884A:E12	ES 155
M00003887C:E09	ES 155
M00003888B:F09	ES 155
M00003891B:H02	ES 155
M00003898C:A01	ES 155
M00003900C:D12	ES 155
M00003906A:C02	ES 155
M00003911C:A09	ES 155
M00003914A:A08	ES 155
M00003915C:D10	ES 155
M00003915C:G08	ES 155
M00003916A:E04	ES 155
M00003926A:F11	ES 155
M00003935B:B01	ES 155
M00003938C:A05	ES 155
M00003942A:D01	ES 155
M00003958C:H08	ES 155
M00003959D:A05	ES 155
M00003960D:C12	ES 155
M00003963D:F01	ES 155
M00003965D:D11	ES 155
M00003968C:G03	ES 155

Clone Name	Tube
M00003970D:H07	ES 155
M00003972C:F07	ES 155
M00003974C:E11	ES 155
M00003974D:E02	ES 155
M00003979B:A04	ES 155
M00003980D:C06	ES 155
M00003985D:B02	ES 155
M00003988D:B01	ES 155
M00003991A:C11	ES 155
M00003993C:D07	ES 155
M00003993D:B03	ES 155
M00003994A:B10	ES 155
M00003996B:H07	ES 155
M00003998B:G10	ES 155
M00004028B:F10	ES 155
M00004029D:A01	ES 155
M00004031C:G06	ES 155
M00004036B:A11	ES 155
M00004036D:C12	ES 155
M00004038A:A04	ES 155
M00004042B:A11	ES 155
M00004047C:B09	ES 155
M00004047D:F12	ES 155
M00004053D:F09	ES 155
M00004054A:D03	ES 155
M00004055C:B10	ES 155
M00004055D:D05	ES 155
M00004057D:G01	ES 155
M00004061B:E05	ES 155
M00004062D:A02	ES 155
M00004066D:G10	ES 155
M00004067B:D03	ES 155
M00004080C:C04	ES 155
M00004085A:H01	ES 155
M00004085B:H02	ES 155
M00004087C:E02	ES 155
M00004093A:C03	ES 155
M00004096D:F02	ES 155
M00004102A:E03	ES 155
M00004103C:E10	ES 155
M00004104A:A12	ES 155
M00004110D:F09	ES 155
M00004114C:D11	ES 155
M00004115A:G12	ES 155
M00004118C:D12	ES 155

Clone Name	Tube
M00004122C:D01	ES 155
M00004134A:A08	ES 155
M00004136C:B12	ES 155
M00004139B:F01	ES 155
M00004141A:D01	ES 155
M00004141B:B01	ES 155
M00004141B:F08	ES 155
M00004143B:B04	ES 155
M00004144D:B02	ES 155
M00004146A:C11	ES 155
M00004146B:E08	ES 155
M00004146C:B04	ES 155
M00004147C:E01	ES 155
M00004151B:A07	ES 155
M00004155A:H03	ES 155
M00004155C:A10	ES 155
M00004158B:E03	ES 155
M00004158D:E08	ES 155
M00004159C:D10	ES 155
M00004159D:F12	ES 155
M00004160D:F06	ES 155
M00004160D:G05	ES 155
M00004162D:F02	ES 156
M00004163B:C03	ES 156
M00004163C:A03	ES 156
M00004164B:E12	ES 156
M00004165C:A11	ES 156
M00004166C:B10	ES 156
M00004169A:E04	ES 156
M00004170A:F03	ES 156
M00004171B:B03	ES 156
M00004172C:A08	ES 156
M00004172D:B12	ES 156
M00004172D:F04	ES 156
M00004175D:E06	ES 156
M00004176C:A09	ES 156
M00004179C:B06	ES 156
M00004179D:A12	ES 156
M00004187B:C02	ES 156
M00004189A:C12	ES 156
M00004192C:B06	ES 156
M00004195A:F07	ES 156
M00004200C:A04	ES 156
M00004201D:C01	ES 156
M00004201D:C03	ES 156

Clone Name	Tube
M00004204C:H08	ES 156
M00004207C:A04	ES 156
M00004208A:D08	ES 156
M00004210A:A03	ES 156
M00004212D:C03	ES 156
M00004214A:E05	ES 156
M00004214D:A05	ES 156
M00004215B:C05	ES 156
M00004220D:C11	ES 156
M00004225D:E03	ES 156
M00004229B:B06	ES 156
M00004230D:B05	ES 156
M00004237C:D10	ES 156
M00004242D:H01	ES 156
M00004245C:G10	ES 156
M00004246B:H07	ES 156
M00004251D:D03	ES 156
M00004263C:D03	ES 156
M00004266B:F07	ES 156
M00004269A:F11	ES 156
M00004269A:G11	ES 156
M00004269B:B04	ES 156
M00004270A:E09	ES 156
M00004276C:A08	ES 156
M00004277D:B02	ES 156
M00004278A:G06	ES 156
M00004278C:B10	ES 156
M00004281A:C04	ES 156
M00004282A:D01	ES 156
M00004282B:D07	ES 156
M00004282C:A12	ES 156
M00004284A:F08	ES 156
M00004295D:C07	ES 156
M00004296B:D03	ES 156
M00004303C:C05	ES 156
M00004310B:E02	ES 156
M00004316A:B03	ES 156
M00004320C:E07	ES 156
M00004321C:C11	ES 156
M00004322B:D03	ES 156
M00004324A:B03	ES 156
M00004324A:D10	ES 156
M00004324A:D05	ES 156
M00004328A:D01	ES 156
M00004330A:A01	ES 156

Clone Name	Tube
M00004336A:A01	ES 156
M00004341C:A09	ES 156
M00004341C:E05	ES 156
M00004344A:G11	ES 156
M00004344D:C12	ES 156
M00004347B:E04	ES 156
M00004347C:A05	ES 156
M00004350A:A04	ES 156
M00004351B:G07	ES 156
M00004352A:D08	ES 156
M00004357B:B06	ES 156
M00004358B:G02	ES 156
M00004359A:E01	ES 156
M00004360C:D09	ES 156
M00004365C:C09	ES 156
M00004365C:G11	ES 156
M00004366D:C11	ES 156
M00004368A:B11	ES 156
M00004372A:E12	ES 156
M00004376D:A12	ES 156
M00004385C:H12	ES 156
M00004393C:D06	ES 156
M00004406A:G09	ES 156
M00004416B:G10	ES 156
M00004418B:A11	ES 156
M00004419A:G02	ES 156
M00004420D:E05	ES 156
M00004430A:A05	ES 156
M00004430B:B10	ES 157
M00004443C:F07	ES 157
M00004462D:D12	ES 157
M00004502A:D12	ES 157
M00004507D:E03	ES 157
M00004509B:B10	ES 157
M00004509D:C06	ES 157
M00004603B:E02	ES 157
M00004603C:C10	ES 157
M00004606D:H09	ES 157
M00004608A:C10	ES 157
M00004608A:H04	ES 157
M00004609A:E09	ES 157
M00023389A:G04	ES 157
M00023394D:D10	ES 157
M00026809A:H08	ES 157
M00026818C:E01	ES 157

Clone Name	Tube
M00026836B:H03	ES 157
M00026842B:A01	ES 157
M00026842D:C02	ES 157
M00026850B:C09	ES 157
M00026856B:G03	ES 157
M00026900A:H07	ES 157
M00026907D:E07	ES 157
M00026910B:G06	ES 157
M00026914C:H09	ES 157
M00026936D:C07	ES 157
M00026961A:B06	ES 157
M00026994D:D07	ES 157
M00027004C:C11	ES 157
M00027017A:B09	ES 157
M00027036A:B06	ES 157
M00027050A:B02	ES 157
M00027052A:E10	ES 157
M00027057C:D10	ES 157
M00027064B:D06	ES 157
M00027081A:A08	ES 157
M00027093A:H02	ES 157
M00027131A:B03	ES 157
M00027159C:F07	ES 157
M00027167C:B10	ES 157
M00027168B:H08	ES 157
M00027170D:C07	ES 157
M00027173C:E11	ES 157
M00027177B:D04	ES 157
M00027178B:A11	ES 157
M00027182B:G06	ES 157
M00027189C:B10	ES 157
M00027193C:A07	ES 157
M00027215A:F06	ES 157
M00027215B:B12	ES 157
M00027244C:B06	ES 157
M00027247C:D02	ES 157
M00027262A:A07	ES 157
M00027270A:D04	ES 157
M00027274A:A09	ES 157
M00027290C:F06	ES 157
M00027291A:G08	ES 157
M00027311A:H09	ES 157
M00027313C:E01	ES 157
M00027314D:E02	ES 157
M00027316C:C03	ES 157

Clone Name	Tube
M00027319C:C03	ES 157
M00027319D:F07	ES 157
M00027332B:H09	ES 157
M00027359B:A06	ES 157
M00027363D:G04	ES 157
M00027364B:E12	ES 157
M00027376C:A02	ES 157
M00027381B:B04	ES 157
M00027400D:H02	ES 157
M00027433B:D12	ES 157
M00027457B:E11	ES 157
M00027459C:B10	ES 157
M00027467A:C07	ES 157
M00027475D:A01	ES 157
M00027480C:E09	ES 157
M00027485C:F07	ES 157
M00027506B:G01	ES 157
M00027513D:F06	ES 157
M00027523A:H05	ES 157
M00027527B:C05	ES 157
M00027549C:G03	ES 157
M00027569A:E05	ES 157
M00027586A:C09	ES 157
M00027589B:G07	ES 157
M00027591A:E04	ES 157
M00027600B:C07	ES 157
M00027605B:D09	ES 157
M00027688C:C01	ES 157
M00027717C:C06	ES 157
M00027724D:D04	ES 157
M00027734D:C03	ES 157
M00027746A:D06	ES 157
M00027801B:D07	ES 157
M00027806C:H05	ES 157
M00028055B:G07	ES 158
M00028063C:H01	ES 158
M00028067A:C11	ES 158
M00028069D:H02	ES 158
M00028070A:H09	ES 158
M00028070D:C03	ES 158
M00028188C:H11	ES 158
M00028193B:E07	ES 158
M00028196A:G03	ES 158
M00028210B:H03	ES 158
M00028211A:F10	ES 158

Clone Name	Tube
M00028212D:C05	ES 158
M00028219B:H05	ES 158
M00028361B:H08	ES 158
M00028366B:B08	ES 158
M00028616C:D09	ES 158
M00028620C:C07	ES 158
M00028763A:G11	ES 158
M00028764B:D03	ES 158
M00028771A:E02	ES 158
M00028773C:C05	ES 158
M00028774D:E10	ES 158
M00028777B:G04	ES 158
M00028782A:F01	ES 158
M00028784A:D12	ES 158
M00028786B:A04	ES 158
M00031370B:C01	ES 158
M00031416D:H05	ES 158
M00031484A:D03	ES 158
M00031485B:G05	ES 158
M00032471D:A05	ES 158
M00032473B:A03	ES 158
M00032474A:G03	ES 158
M00032475A:A06	ES 158
M00032489B:G12	ES 158
M00032490D:E08	ES 158
M00032494C:H08	ES 158
M00032497D:B10	ES 158
M00032504B:B10	ES 158
M00032507D:G08	ES 158
M00032508A:E03	ES 158
M00032515A:B12	ES 158
M00032517C:E10	ES 158
M00032519D:F08	ES 158
M00032534B:E12	ES 158
M00032541C:G03	ES 158
M00032553A:A07	ES 158
M00032556D:A03	ES 158
M00032562C:F01	ES 158
M00032567B:G05	ES 158
M00032568B:F08	ES 158
M00032577D:F01	ES 158
M00032580D:A09	ES 158
M00032581B:A09	ES 158
M00032584A:D06	ES 158
M00032586C:B04	ES 158

Clone Name	Tube
M00032590B:H01	ES 158
M00032594C:F05	ES 158
M00032597A:H02	ES 158
M00032605B:D09	ES 158
M00032613A:E11	ES 158
M00032614C:B10	ES 158
M00032614D:D08	ES 158
M00032620B:F06	ES 158
M00032621A:F11	ES 158
M00032628C:B06	ES 158
M00032634B:D09	ES 158
M00032637A:F09	ES 158
M00032638B:F02	ES 158
M00032644C:B05	ES 158
M00032645D:C01	ES 158
M00032647B:F06	ES 158
M00032652C:C07	ES 158
M00032666A:C02	ES 158
M00032671B:D06	ES 158
M00032671B:D08	ES 158
M00032676C:C10	ES 158
M00032688C:A03	ES 158
M00032700A:E09	ES 158
M00032707D:F08	ES 158
M00032711B:F01	ES 158
M00032723D:H02	ES 158
M00032727A:E04	ES 158
M00032728D:F01	ES 158
M00032729A:F10	ES 158
M00032733B:F12	ES 158
M00032734B:E12	ES 158
M00032734C:C05	ES 158
M00032749D:G03	ES 158
M00032753A:C07	ES 158
M00032759A:A03	ES 158
M00032765A:C05	ES 158
M00032770C:G11	ES 158
M00032772D:D03	ES 158
M00032773D:F08	ES 158
M00032774C:C04	ES 158
M00032787D:C05	ES 159
M00032791B:H11	ES 159
M00032791D:F01	ES 159
M00032792C:B01	ES 159
M00032793A:G06	ES 159

Clone Name	Tube
M00032795C:A03	ES 159
M00032797D:D08	ES 159
M00032825B:F08	ES 159
M00032826C:D10	ES 159
M00032828A:A06	ES 159
M00032829D:A05	ES 159
M00032830D:D02	ES 159
M00032831A:C07	ES 159
M00032831A:E09	ES 159
M00032835D:G04	ES 159
M00032836B:A07	ES 159
M00032848D:B10	ES 159
M00032892C:C12	ES 159
M00032908A:D08	ES 159
M00032918D:B04	ES 159
M00032928C:D02	ES 159
M00032944A:B07	ES 159
M00032945D:B07	ES 159
M00032979D:C11	ES 159
M00032979D:H07	ES 159
M00032985D:G09	ES 159
M00032987B:F01	ES 159
M00032988B:G01	ES 159
M00033006A:F10	ES 159
M00033028C:A02	ES 159
M00033028D:C10	ES 159
M00033037B:F04	ES 159
M00033041A:B11	ES 159
M00033055D:D02	ES 159
M00033071C:G05	ES 159
M00033071D:E08	ES 159
M00033072A:A09	ES 159
M00033080C:A07	ES 159
M00033081D:D11	ES 159
M00033144A:D02	ES 159
M00033146D:A03	ES 159
M00033147C:B08	ES 159
M00033149B:E10	ES 159
M00033150B:E02	ES 159
M00033150C:A11	ES 159
M00033183B:F10	ES 159
M00033218C:F07	ES 159
M00033223C:G04	ES 159
M00033230C:G10	ES 159
M00033232B:C08	ES 159

Clone Name	Tube
M00033246A:H12	ES 159
M00033248D:H11	ES 159
M00033264B:E06	ES 159
M00033274D:F03	ES 159
M00033311B:G10	ES 159
M00033324B:F04	ES 159
M00033326B:B05	ES 159
M00033329C:C02	ES 159
M00033296C:C11	ES 159
M00033302A:E11	ES 159
M00033302B:F10	ES 159
M00033303C:F09	ES 159
M00033342B:F03	ES 159
M00033344A:B06	ES 159
M00033359C:H05	ES 159
M00033360C:A03	ES 159
M00033374D:C07	ES 159
M00033413A:A08	ES 159
M00033420B:E08	ES 159
M00033434D:F05	ES 159
M00033441A:B12	ES 159
M00033445D:G03	ES 159
M00038290A:D12	ES 159
M00038304B:E02	ES 159
M00038389D:D10	ES 159
M00038390B:F02	ES 159
M00038616C:C09	ES 159
M00038616D:B07	ES 159
M00038618D:D08	ES 159
M00038619B:F09	ES 159
M00038619D:C12	ES 159
M00039001A:B10	ES 159
M00039024D:E12	ES 159
M00039055C:A01	ES 159
M00039056B:G01	ES 159
M00039063C:H09	ES 159
M00039067A:C05	ES 159
M00039067B:F07	ES 159
M00039076D:G04	ES 159
M00039078B:B03	ES 159
M00039078D:C10	ES 159
M00039081B:C04	ES 159
M00039081B:G07	ES 159
M00039100A:G04	ES 159
M00039105D:A08	ES 159

Clone Name	Tube
M00039107A:E12	ES 159
M00039111A:C12	ES 160
M00039121D:E07	ES 160
M00039124D:H01	ES 160
M00039125D:H12	ES 160
M00039131C:B09	ES 160
M00039133B:D06	ES 160
M00039133C:F12	ES 160
M00039134D:F08	ES 160
M00039138B:G05	ES 160
M00039140A:F05	ES 160
M00039143A:F04	ES 160
M00039143D:C10	ES 160
M00039146B:G04	ES 160
M00039162D:C04	ES 160
M00039165D:C04	ES 160
M00039175A:F01	ES 160
M00039204A:E09	ES 160
M00039207A:F07	ES 160
M00039219B:C08	ES 160
M00039222B:A04	ES 160
M00039225A:D11	ES 160
M00039246B:A08	ES 160
M00039248C:A08	ES 160
M00039251C:H12	ES 160
M00039251D:B08	ES 160
M00039255D:B01	ES 160
M00039258C:C01	ES 160
M00039270D:D02	ES 160
M00039275B:E02	ES 160
M00039278C:D03	ES 160
M00039284D:H07	ES 160
M00039285B:G04	ES 160
M00039291D:F02	ES 160
M00039294C:B09	ES 160
M00039302B:E10	ES 160
M00039326A:G07	ES 160
M00039326C:B08	ES 160
M00039331B:F09	ES 160
M00039338B:F07	ES 160
M00039344C:A11	ES 160
M00039349D:B11	ES 160
M00039381C:C07	ES 160
M00039383A:H07	ES 160
M00039411D:D09	ES 160

Clone Name	Tube
M00039413C:E06	ES 160
M00039430A:E04	ES 160
M00039433B:D06	ES 160
M00039433C:E03	ES 160
M00039438B:D08	ES 160
M00039440C:G06	ES 160
M00039457D:C02	ES 160
M00039471D:G10	ES 160
M00039472B:E05	ES 160
M00039478C:B02	ES 160
M00039554D:B09	ES 160
M00039556C:G05	ES 160
M00039559B:C07	ES 160
M00039560B:G09	ES 160
M00039560C:G06	ES 160
M00039617C:A10	ES 160
M00039654C:C11	ES 160
M00039668C:F01	ES 160
M00039672C:D05	ES 160
M00039686C:C01	ES 160
M00039694C:H01	ES 160
M00039698C:B03	ES 160
M00039710B:A01	ES 160
M00039710B:E01	ES 160
M00039785C:H12	ES 160
M00039786D:A10	ES 160
M00039805B:B06	ES 160
M00039806B:D05	ES 160
M00039820B:F06	ES 160
M00039822A:H02	ES 160
M00039826B:F09	ES 160
M00039826D:E04	ES 160
M00039828B:H06	ES 160
M00039829B:E01	ES 160
M00039860B:E01	ES 160
M00039860D:B02	ES 160
M00039861C:B12	ES 160
M00039865A:C09	ES 160
M00039869A:H01	ES 160
M00039871C:G05	ES 160
M00039873B:H04	ES 160
M00039874A:B06	ES 160
M00039885C:D11	ES 160
M00039894C:D09	ES 160
M00039895D:C04	ES 160

Clone Name	Tube
M00039900B:G04	ES 160
M00039915B:E08	ES 160
M00039921A:B10	ES 160
M00004824A:D12	ES 160
M00004824D:H05	ES 160
M00004831C:G11	ES 160
M00004832D:G04	ES 160
M00004836B:C02	ES 161
M00004839B:C12	ES 161
M00004843A:G12	ES 161
M00004846A:A10	ES 161
M00004850A:B02	ES 161
M00004852D:C06	ES 161
M00004856D:F09	ES 161
M00004873B:G04	ES 161
M00004876B:A06	ES 161
M00005002A:C03	ES 161
M00005003D:C02	ES 161
M00005013D:H05	ES 161
M00005014B:F02	ES 161
M00005016C:E04	ES 161
M00005309B:A11	ES 161
M00005314A:G10	ES 161
M00005332A:C06	ES 161
M00005333D:D08	ES 161
M00005346D:A03	ES 161
M00005349C:C02	ES 161
M00005359B:B08	ES 161
M00005359B:D09	ES 161
M00005364B:E10	ES 161
M00005365A:F05	ES 161
M00005366D:F08	ES 161
M00005367D:A11	ES 161
M00005375D:A10	ES 161
M00005379A:D10	ES 161
M00005380B:H10	ES 161
M00005383A:C11	ES 161
M00005385A:B12	ES 161
M00005385D:F07	ES 161
M00005387A:B03	ES 161
M00005392A:G06	ES 161
M00005401D:F09	ES 161
M00005403C:A01	ES 161
M00005405C:D01	ES 161
M00005409D:B02	ES 161

Clone Name	Tube
M00005413D:A05	ES 161
M00005422B:B08	ES 161
M00005422D:H02	ES 161
M00005422D:H10	ES 161
M00005423A:C11	ES 161
M00005423C:A10	ES 161
M00005423C:D07	ES 161
M00005434A:C03	ES 161
M00005442A:B10	ES 161
M00005445A:E07	ES 161
M00005445D:D04	ES 161
M00005445D:F11	ES 161
M00005452B:G03	ES 161
M00005452D:E05	ES 161
M00005460D:C11	ES 161
M00005461A:D12	ES 161
M00005463A:G02	ES 161
M00005466C:B01	ES 161
M00005468A:C04	ES 161
M00005468D:C01	ES 161
M00005474C:H09	ES 161
M00005485C:H04	ES 161
M00005489B:C08	ES 161
M00005500A:D04	ES 161
M00005504C:F12	ES 161
M00005504D:F06	ES 161
M00005505A:F01	ES 161
M00005505B:E01	ES 161
M00005506C:E09	ES 161
M00005506D:E11	ES 161
M00005507B:A03	ES 161
M00005511A:F05	ES 161
M00005512B:H01	ES 161
M00005515D:F02	ES 161
M00005520B:E01	ES 161
M00005520B:H05	ES 161
M00005524C:H04	ES 161
M00005535B:B01	ES 161
M00005540A:F09	ES 161
M00005557D:H10	ES 161
M00005569D:G09	ES 161
M00005570A:B08	ES 161
M00005570A:D05	ES 161
M00005603B:H03	ES 161
M00005606D:B12	ES 161

Clone Name	Tube
M00005607B:C04	ES 161
M00005616B:F07	ES 161
M00005622A:H02	ES 161
M00005623B:G01	ES 161
M00005626D:G11	ES 161
M00005634A:F07	ES 161
M00005641B:E09	ES 161
M00005643D:A05	ES 161
M00005674C:F04	ES 161
M00005675D:D09	ES 161
M00005689C:B02	ES 161
M00005703B:E03	ES 161
M00005703D:G10	ES 161
M00005710B:H03	ES 162
M00005743D:A12	ES 162
M00005763D:A01	ES 162
M00005766D:D12	ES 162
M00005771D:C02	ES 162
M00005819D:F09	ES 162
M00005822C:A04	ES 162
M00006576D:C02	ES 162
M00006577A:H10	ES 162
M00006582D:A09	ES 162
M00006585A:D07	ES 162
M00006585A:F09	ES 162
M00006586D:D04	ES 162
M00006592A:A12	ES 162
M00006595B:C10	ES 162
M00006601D:G05	ES 162
M00006631C:A04	ES 162
M00006631D:D02	ES 162
M00006636B:E04	ES 162
M00006641B:F05	ES 162
M00006646A:A07	ES 162
M00006678A:A03	ES 162
M00006678C:C02	ES 162
M00006712C:H01	ES 162
M00006714C:D06	ES 162
M00006738A:F12	ES 162
M00006739B:A04	ES 162
M00006740B:A09	ES 162
M00006743A:D04	ES 162
M00006743A:H11	ES 162
M00006756B:G06	ES 162
M00006756C:A02	ES 162

Clone Name	Tube
M00006861D:H10	ES 162
M00006872D:B07	ES 162
M00006877B:C09	ES 162
M00006877C:F11	ES 162
M00006884D:A08	ES 162
M00006885A:F07	ES 162
M00006890C:F10	ES 162
M00006904D:A02	ES 162
M00006907A:C09	ES 162
M00006907B:C06	ES 162
M00006989B:G05	ES 162
M00006994C:F06	ES 162
M00007002C:A10	ES 162
M00007006C:C12	ES 162
M00007007A:E04	ES 162
M00007031A:E02	ES 162
M00007032A:B05	ES 162
M00007032C:A12	ES 162
M00007046D:C09	ES 162
M00007048B:E11	ES 162
M00007048C:A12	ES 162
M00007059B:D07	ES 162
M00007060D:G07	ES 162
M00007064D:D12	ES 162
M00007070C:C01	ES 162
M00007081B:C08	ES 162
M00007081B:E09	ES 162
M00007082D:E05	ES 162
M00007098A:E10	ES 162
M00007103C:C12	ES 162
M00007103D:C02	ES 162
M00007112D:D03	ES 162
M00007117A:C11	ES 162
M00007126A:A02	ES 162
M00007141C:B05	ES 162
M00007154A:E06	ES 162
M00007155C:D07	ES 162
M00007155D:C09	ES 162
M00007158D:D03	ES 162
M00007178A:C02	ES 162
M00007195C:E11	ES 162
M00007197B:B05	ES 162
M00007202B:F01	ES 162
M00007947A:B06	ES 162
M00007953D:F07	ES 162

Clone Name	Tube
M00007969D:C01	ES 162
M00007973B:D11	ES 162
M00007975C:A10	ES 162
M00007975D:F12	ES 162
M00007980A:B01	ES 162
M00007980B:A07	ES 162
M00007981C:F07	ES 162
M00007985C:D08	ES 162
M00008001B:F05	ES 162
M00008007B:E03	ES 162
M00008016B:E09	ES 162
M00008019B:A01	ES 162
M00008020D:D05	ES 162
M00008020D:F02	ES 162
M00008021C:G12	ES 162
M00008045C:A05	ES 162
M00008055D:G03	ES 162
M00008059B:F08	ES 162
M00008059D:B08	ES 162
M00008065D:A07	ES 163
M00008071D:H03	ES 163
M00008073A:D01	ES 163
M00008073D:D01	ES 163
M00021649B:A02	ES 163
M00021650D:A11	ES 163
M00021653A:B02	ES 163
M00021668D:A03	ES 163
M00021676C:G03	ES 163
M00021677A:D09	ES 163
M00021678A:H03	ES 163
M00021678D:H04	ES 163
M00021681C:C09	ES 163
M00021690A:C03	ES 163
M00021697C:B07	ES 163
M00021700D:H03	ES 163
M00021852C:H02	ES 163
M00021855D:F10	ES 163
M00021866C:H08	ES 163
M00021896D:A05	ES 163
M00021923A:B12	ES 163
M00021923D:H02	ES 163
M00021933B:F02	ES 163
M00021941A:D09	ES 163
M00021952B:G06	ES 163
M00021958B:E08	ES 163

Clone Name	Tube
M00021967D:H06	ES 163
M00021971C:B11	ES 163
M00021974D:F01	ES 163
M00021981A:C02	ES 163
M00021991D:F09	ES 163
M00021998B:D09	ES 163
M00022009C:A08	ES 163
M00022016B:F01	ES 163
M00022032A:G05	ES 163
M00022051B:D07	ES 163
M00022069D:C12	ES 163
M00022070B:B04	ES 163
M00022073C:C07	ES 163
M00022081A:B07	ES 163
M00022088B:F10	ES 163
M00022088B:H02	ES 163
M00022088D:E10	ES 163
M00022090B:A10	ES 163
M00022092D:A11	ES 163
M00022094B:G02	ES 163
M00022096D:A03	ES 163
M00022103C:D05	ES 163
M00022104A:G08	ES 163
M00022117C:A02	ES 163
M00022118A:E06	ES 163
M00022140D:A07	ES 163
M00022144C:E12	ES 163
M00022158B:B09	ES 163
M00022170C:C01	ES 163
M00022171A:F03	ES 163
M00022185A:B03	ES 163
M00022193B:A09	ES 163
M00022193C:C09	ES 163
M00022200B:B05	ES 163
M00022202C:C04	ES 163
M00022208B:D03	ES 163
M00022208C:E04	ES 163
M00022208C:F08	ES 163
M00022212D:G02	ES 163
M00022216D:D10	ES 163
M00022218B:B12	ES 163
M00022220A:A07	ES 163
M00022224A:C07	ES 163
M00022224A:G07	ES 163
M00022228B:B11	ES 163

Clone Name	Tube
M0002229D:E01	ES 163
M00022237C:E04	ES 163
M00022237D:D06	ES 163
M00022238C:G04	ES 163
M00022240B:C12	ES 163
M00022240D:B11	ES 163
M00022249D:C01	ES 163
M00022250A:B04	ES 163
M00022262A:F06	ES 163
M00022262B:B06	ES 163
M00022264A:B02	ES 163
M00022265A:F11	ES 163
M00022269C:A04	ES 163
M00022273A:E03	ES 163
M00022282B:C09	ES 163
M00022305A:B04	ES 163
M00022363C:D05	ES 163
M00022367D:G11	ES 163
M00022368A:B11	ES 163
M00022372D:H12	ES 163
M00022374C:E11	ES 163
M00022376D:D05	ES 163
M00022383C:A12	ES 163
M00022386D:F10	ES 163
M00022392B:F01	ES 163
M00022403C:E12	ES 164
M00022415C:D12	ES 164
M00022416D:D01	ES 164
M00022421A:F12	ES 164
M00022425A:C09	ES 164
M00022430C:C06	ES 164
M00022435B:G12	ES 164
M00022436C:F11	ES 164
M00022438C:H09	ES 164
M00022442B:G03	ES 164
M00022446C:H06	ES 164
M00022449D:F08	ES 164
M00022452B:E06	ES 164
M00022454C:B08	ES 164
M00022457A:G05	ES 164
M00022467D:B03	ES 164
M00022470D:B02	ES 164
M00022472D:B01	ES 164
M00022474B:C08	ES 164
M00022475D:C07	ES 164

Clone Name	Tube
M00022481B:A04	ES 164
M00022485B:E07	ES 164
M00022487B:A08	ES 164
M00022487C:C02	ES 164
M00022491A:A08	ES 164
M00022491D:A10	ES 164
M00022494B:D06	ES 164
M00022494D:A05	ES 164
M00022499D:D08	ES 164
M00022507C:C08	ES 164
M00022509A:H02	ES 164
M00022509B:D11	ES 164
M00022512B:A09	ES 164
M00022516B:C05	ES 164
M00022525B:D09	ES 164
M00022530B:C04	ES 164
M00022537B:C06	ES 164
M00022546B:E05	ES 164
M00022559D:G10	ES 164
M00022563B:C08	ES 164
M00022590B:E05	ES 164
M00022600D:B05	ES 164
M00022601B:G06	ES 164
M00022618B:D09	ES 164
M00022618C:E04	ES 164
M00022627B:H03	ES 164
M00022634A:C07	ES 164
M00022634B:H09	ES 164
M00022638A:D03	ES 164
M00022642A:G08	ES 164
M00022648A:D08	ES 164
M00022656D:D07	ES 164
M00022662C:H04	ES 164
M00022662D:H03	ES 164
M00022672C:H04	ES 164
M00022674C:H08	ES 164
M00022677C:C01	ES 164
M00022678B:C08	ES 164
M00022681D:E10	ES 164
M00022682D:A10	ES 164
M00022684A:E06	ES 164
M00022690A:A07	ES 164
M00022694A:F05	ES 164
M00022696B:C11	ES 164
M00039921C:H11	ES 164

Clone Name	Tube
M00039929B:E06	ES 164
M00039929D:H10	ES 164
M00039932B:A07	ES 164
M00039976C:F11	ES 164
M00039977B:D12	ES 164
M00039981D:B01	ES 164
M00040003A:G10	ES 164
M00040016C:E07	ES 164
M00040023B:B10	ES 164
M00040025A:B04	ES 164
M00040034A:E06	ES 164
M00040034B:G02	ES 164
M00040041A:G08	ES 164
M00040041D:F01	ES 164
M00040045B:H07	ES 164
M00040061C:C08	ES 164
M00040075B:A05	ES 164
M00040078A:C07	ES 164
M00040079B:F06	ES 164
M00040079D:D09	ES 164
M00040081C:E02	ES 164
M00040094B:C08	ES 164
M00040118D:C05	ES 164
M00040123C:A10	ES 164
M00040127C:D02	ES 164
M00022698C:D10	ES 164
M00022702D:E02	ES 164
M00022703D:B11	ES 164
M00022706D:G08	ES 164
M00022727A:G01	ES 164
M00022738D:G08	ES 164
M00022740C:H11	ES 165
M00022797D:A06	ES 165
M00022801D:D09	ES 165
M00022805B:A10	ES 165
M00022812A:G01	ES 165
M00022820A:F07	ES 165
M00022835C:A09	ES 165
M00022854C:G07	ES 165
M00022856D:A07	ES 165
M00022857B:A09	ES 165
M00022897B:F06	ES 165
M00022901A:C05	ES 165
M00022904C:D04	ES 165
M00022924B:A05	ES 165

Clone Name	Tube
M00022924C:F04	ES 165
M00022945A:H09	ES 165
M00022945B:F11	ES 165
M00022947B:D02	ES 165
M00022952A:B02	ES 165
M00022953B:D06	ES 165
M00022964A:B03	ES 165
M00022972C:E05	ES 165
M00022992A:H06	ES 165
M00022992B:G12	ES 165
M00022995C:G07	ES 165
M00023004C:A01	ES 165
M00023007D:D03	ES 165
M00023020C:H03	ES 165
M00023097D:B08	ES 165
M00039184D:H09	ES 165
M00039364D:E05	ES 165
M00039377B:E05	ES 165
M00039377B:H09	ES 165
M00039483A:D10	ES 165
M00039526A:A08	ES 165
M00039537A:F08	ES 165
M00039564D:D04	ES 165
M00039594C:B06	ES 165
M00039598A:E04	ES 165
M00039630D:B07	ES 165
M00039642A:A08	ES 165
M00039642C:F08	ES 165
M00039646A:E06	ES 165
M00039647A:A02	ES 165
M00039647B:A02	ES 165
M00039739B:H12	ES 165
M00040132A:H09	ES 165
M00040162A:E02	ES 165
M00040169A:G06	ES 165
M00040173D:A04	ES 165
M00040174D:G06	ES 165
M00040198A:F12	ES 165
M00040224C:F06	ES 165
M00040247D:D02	ES 165
M00040252C:G05	ES 165
M00040267D:A12	ES 165
M00040287A:C11	ES 165
M00040287C:F10	ES 165
M00040289D:C06	ES 165

Clone Name	Tube
M00039747B:B06	ES 165
M00039748C:G09	ES 165
M00040201A:H01	ES 165
M00040219B:B07	ES 165
M00040291A:G10	ES 165
M00040298B:B09	ES 165
M00040314B:D07	ES 165
M00040326B:G09	ES 165
M00040329A:H05	ES 165
M00040338A:B10	ES 165
M00040344C:D05	ES 165
M00040349D:D07	ES 165
M00040351A:C08	ES 165
M00040351D:G07	ES 165
M00040366B:H10	ES 165
M00040367A:C08	ES 165
M00040381A:B06	ES 165
M00040384B:E04	ES 165
M00040391A:G05	ES 165
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CLAIMS

We claim:

1. A library of polynucleotides, the library comprising the sequence information of at least one of SEQ ID NO:1-3351.
2. The library of claim 1, wherein the library is provided on a nucleic acid array.
3. The library of claim 1, wherein the library is provided in a computer-readable format.
4. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in a cancer cell of high metastatic potential relative to a control cell, wherein the control cell is a normal cell or a cell of low metastatic potential, wherein the expression is greater in the metastatic tissue, and wherein the sequence is selected from the group consisting of SEQ ID NOs:14, 137, 151, 152, 171, 200, 254, 262, 271, 348, 412, 472, 507, 520, 530, 588, 623, 637, 660, 678, 680, 700, 714, 774, 812, 834, 901, 937, 976, 1168, 1333, 1352, 1520, 1524, 1546, 1550, 1574, 1580, 1590, 1599, 1607, 1622, 1706, 1752, 1768, 1769, 1780, 1781, 1799, 1803, 1811, 1851, 1856, 1867, 1872, 1875, 1884, 1919, 1923, 1939, 1975, 2024, 2045, 2060, 2071, 2118, 2119, 2128, 2135, 2177, 2181, 2184, 2185, 2190, 2193, 2232, 2239, 2283, 2311, 2314, 2338, 2378, 2393, 2394, 2395, 2398, 2460, 2490, 2505, 2514, 2540, 2542, 2597, 2607, 2640, 2657, 2669, 2670, 2674, 2679, 2684, 2707, 2724, 2757, 2776, 2804, 2818, 2906, 2959, 2964, 2968, 2976, 2980, 2987, 3010, 3043, 3047, 3050, 3071, 3072, 3092, 3095, 3097, 3140, 3157, 3173, 3187, 3203, 3210, 3212, 3220, 3236, 3249, 3264, 3284, 3288, 3305, 3309, 3318, 3330, 3331, and 3335.
5. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal colon tissue relative to colon cancer tissue, wherein the expression is greater in the cancer tissue, and wherein the sequence is selected from the group consisting of SEQ ID NOs:7, 164, 734, 836, 928, 965, 987, 1026, 1044, 1119, 1226, 1227, 1251, 1316, 1429, 1442, 1540, 1553, 1560, 1577, 1588, 1610, 1620, 1626, 1673, 2416, 2749, 2976, 3129 and 3132.

6. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal colon tissue relative to colon cancer tissue, wherein the expression is greater in normal tissue than cancer tissue, and wherein the sequence is selected from the group consisting of SEQ ID NOs:105, 198, 465, 489, 745, 859, 976, 1011, 1045, 1138, 1226, 1251, 1253, 1392, 1474, 1559, 1571, 1589, 1591, 1607, 1608, 1643, 1753, 1764, 1766, 1782, 1811, 2749, 2784, 2790, 2805, 2976, 3128, 3129, 3146, 3150, and 3151.

7. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal human prostate cells relative to human prostate cancer cells, wherein the expression is greater in normal cells than cancer cells, and wherein the sequence is selected from the group consisting of SEQ ID NOs:53, 446, 1410, 1754, 1801, 1845, 2060, 2143, 2632, 2899, and 3338.

8. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal human prostate cells relative to human prostate cancer cells, wherein the expression is greater in cancer cells than normal cells, and wherein the sequence is selected from the group consisting of SEQ ID NOs:86, 93, 687, 1269, 1581, 1647, 1649, 1710, 1717, 1772, 1960, 2987, 3128, 3132, 3150, 3222, and 3268.

9. An isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of SEQ ID NOs:1-3351 or a degenerate variant or fragment thereof.

10. A recombinant host cell containing the polynucleotide of claim 9.

11. An isolated polypeptide encoded by the polynucleotide of claim 9.

12. An antibody that specifically binds a polypeptide of claim 11.

13. A vector comprising the polynucleotide of claim 9.

14. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:
detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, wherein the gene product is encoded by a

gene corresponding to a sequence of at least one of SEQ ID NOs: 14, 137, 151, 152, 171, 200, 254, 262, 271, 348, 412, 472, 507, 520, 530, 588, 623, 637, 660, 678, 680, 700, 714, 774, 812, 834, 901, 937, 976, 1168, 1333, 1352, 1520, 1524, 1546, 1550, 1574, 1580, 1590, 1599, 1607, 1622, 1706, 1752, 1768, 1769, 1780, 1781, 1799, 1803, 1811, 1851, 1856, 1867, 1872, 1875, 1884, 1919, 1923, 1939, 1975, 2024, 2045, 2060, 2071, 2118, 2119, 2128, 2135, 2177, 2181, 2184, 2185, 2190, 2193, 2232, 2239, 2283, 2311, 2314, 2338, 2378, 2393, 2394, 2395, 2398, 2460, 2490, 2505, 2514, 2540, 2542, 2597, 2607, 2640, 2657, 2669, 2670, 2674, 2679, 2684, 2707, 2724, 2757, 2776, 2804, 2818, 2906, 2959, 2964, 2968, 2976, 2980, 2987, 3010, 3043, 3047, 3050, 3071, 3072, 3092, 3095, 3097, 3140, 3157, 3173, 3187, 3203, 3210, 3212, 3220, 3236, 3249, 3264, 3284, 3288, 3305, 3309, 3318, 3330, 3331, and 3335.

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

15. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, wherein the gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOs: 7, 164, 734, 836, 928, 965, 987, 1026, 1044, 1119, 1226, 1227, 1251, 1316, 1429, 1442, 1540, 1553, 1560, 1577, 1588, 1610, 1620, 1626, 1673, 1960, 2416, 2749, 2976, 2987, 3128, 3129, 3132, 3150, 3222, and 3268.

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

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